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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Lin, L., Jin, L., Lin, X., Voros, A., Underhill, P. and Mignot, E. Direct Submission
Submitted (12-JAN-1998) Psychiatry and Behavioral Sciences, Stanford University, Lab Surge Building, 1201 Welch Road, RC P126, Palo Alto, CA 94304, USA
                                                                                                                                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 73)
Lin,L., Jin,L., Kimura,A., Carrington,M. and Mignot,E.
DQ microsatellite association studies in three ethnic groups
Tissue Antigens 50 (5), 507-520 (1997)
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 85)
1 (bases 1, La Bella, F. and Heintz, N. Gallinari, P., La Bella, F. and Heintz, N. Characterization and purification of HITF2, a novel CCAAT-binding protein that interacts with a histone Hl subtype-specific consensuals.
                                                                                                                                                                                                   2 (bases 1 to 73)
2 (bases 1 to 73)
Lin,L., Jin,K., Voros,A., Underhill,P. and Mignot,E.
Microsatellite single nucleotide polymorphisms in the HLA-DQ
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Bukheria; Primates; Catarrhini; Hominidae; Homo.

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Lin,L., Jin,L., Kimura,A., Carrington,M. and Mignot,E.

DQ microsatellite association studies in three ethnic groups

Tissue Antigens 50 (5), 507-520 (1997)
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Lin,L., Jin,L., Lin,X., Voros,A., Underhill,P.
Microsatellite single nucleotide polymorphisms
Tissue Antigens 52 (1), 9-18 (1998)
98378271
            AF042302 77 bp
Homo sapiens chromosome
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AF042302.1 GI:4191289
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Submitted (12-JAN-1998) Psychiatry and Behavioral Sciences, Stanford University, Lab Surge Building, 1201 Welch Road, R P126, Palo Alto, CA 94304, USA
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Submitted (12-JAN-1998) Psychiatry and Behavioral Sciences, Stanford University, Lab Surge Building, 1201 Welch Road, Room P126, Palo Alto, CA 94304, USA
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                                                 Utah, Dept. of Human Genetics
2160 Eccles Institute of Human Genetics
Salt Lake City, UT 84112
e-mail: sts@corona.med.utah.edu
primer A: GATCGAGAGCAGCCTGGA
primer B: TGGTGATTTGAAGGAATGCC
                                                                                                                                                                              Genetic and physical mapping of simple sequence sequence tagged sites from the human genome Unpublished (1994)
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1 (bases 1 to 77)

1 (bases 1 to 77)

Gerken, S. C., Matsunami, N., Plaetke, R.; Albertsen, H., Ballard, L., Melis, R., Lawrence, E., Moore, M., Holik, P.R., Carlson, M., Zhao, X., Robertson, M., Bradley, P., Elsner, T., Tingey, A., Lalouel, J.-M. and
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                                                                                                                                                                Submitted by: Utah Center for Human Genome Research University
                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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Initial Denaturation:
                 PCR Profile:
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                              to Label: Primer
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31 c 3
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three ethnic
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DEFINITION ACCESSION

sequence,

AU025275 97 Rattus norvegicus,

97 bp DNA rvegicus, OTSUKA clone, sequence tagged site.

STS OT48.13/788f08;

02-MAR-1999

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W.musculus D4nds1 m

X55208

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micro--
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                                                                                                    l Similarity
39; Conserv
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40; Conserv
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Cornall, R.J., Altman, T.J., Hearne, C.M. and Todd, J.A.
The generation of a library of PCR-analyzed microsatellite
for genetic mapping of the mouse genome
Genomics 10 (4), 874-881 (1991)
                                                                                                                                                                                                                                                                                                                                                                             Submitted (20-OCT-1990)
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Vertebrata; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 97)
Hearne, C.M.
Direct Submission
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                                                                                                    0.1%; Score 39; DB 12; larity 100.0%; Pred. No. 3.5e-08; Conservative 0; Mismatches 0;
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                                                                                                                                                                               /organism="Mus musculus"
/strain="NOD"
/db_xref="taxon:10090"
/chromosome="4"
/map="45 cM"
a 27 c 6 g 23
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100.0%; Pred. No. 1.1e-08;
tive 0; Mismatches 0;
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Rattus norvegicus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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I31337
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STS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The large-scale mapping of rat microsatellite markers Unpublished (1998)
2 (bases 1 to 97)
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                                                                                                                                                                                                                                            tength polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences
method of using the same
patent: US 5582979-A 249 10-DEC-1996;
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249 from patent
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100.0%; Pred. No. 1.2e-07;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 87)
Cornall.R.J., Altman,T.J., Hearne,C.M. and Todd,J.A.
The generation of a library of PCR-analyzed microsatellite variants for genetic mapping of the mouse genome
Genomics 10 (4), 874-881 (1991)
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                                                    38;
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Sequence 325 from patent US 5582979.
131413
                                                                                                                                                                                                                        Submitted (22-OCT-1990) C.M. Hearne, UNIVERSITY OF OXFORD, NUFFI DEPT. SURGERY, LEVEL 6, JOHN RADCLIFFE HOSP., HEADINGTON OXFORD, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                            microsatellite DNA. house mouse.
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                                                                                                                                                                                                                                                                                Hearne, C.M.
                                                                Similarity
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Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 100)
                                                                                     Wang,X., Tolstonog,G., Shoeman,R.L. and Traub,P
Selective binding of specific mouse genomic DNA
vimentin filaments in vitro
DNA Cell Biol. 15 (3), 209-225 (1996)
                                                                                                                                          Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 102)
                                                                                                                                                                                                                                             M.musculus
X89128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Weissenbach, J., Gyapay, G., Dib, C., Vignal, A., Millasseau, P., Vaysseix, G. and Lathrop, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (05-OCT-1992) Genethon, B.P. E-mail: Jean Weissenbach@genethon.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STS; CA repeat; dinucleotide repeat; GT repeat; microsatellite marker; repeat polymorphism.
Submitted (23-JUN-1995) Shoeman R. L., Max-Planck-Institute fuer zellbiologie, Rosenhof, Ladenburg, Germany, D-68526
                             Shoeman, R.L.
Direct Submission
                                                                         96226400
                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                               X89128.1 GI:872135
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/db_xref="taxon:9606"
/chromosome="1"
/cell_line="CEPH 134702"
/clone_lib="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (11-DEC-1998) to the DDBJ/EMBL/GenBank databases. Takeshi K Watanabe, Otsuka GEN Research Institute, Otsuka Pharmaceutical Co., Ltd; 463-10, Kagasuno, Kawauchi-cho, Tokushima, Tokushima, Tokushima (71-0192, Japan (E-mail:watanabe@otsuka.gr.jp, Tel:+81-886-65-2888, Fax:+81-886-37-1035)
                                                                                                                                                                                                                                                                                                                                                                                                                       Watanabe, T.K., Hishigaki, H., Okuno, S., Mizoguchi, A., Tsuji, A., Ono, T., Yamasaki, Y., Kanemoto, N., Takahash. Nakamura, Y., Takagi, Y. and Tanigami, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus, OT sequence tagged site.
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                            /tissue_type="liver"
/note="109c04F=5'.-CCCTTTCCTATTTTC-3',
109c04R=5'.-AATTAAAGTATAAGGAAATACACAT-3'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="d(CA/GT)n dinucleotide repeats"
/rpt_unit=14. .15
/function="recombination, potentially to for
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/db_xref="taxon:10090"
                                                                                                                                          /cell_type="hepatocyte"
/clone="109c04"
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                                                                                                                                                                                            /organism="Rattus norvegicus"
/strain="Brown Norway"
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/function="sequence bound
/evidence=experimental
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AF042298
AF042298.1
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Lin, L., Jin, L., Lin, X., Voros, A., Underhill, P. and Mignot, E. Direct Submission
Submitted (12-JN-1998) Psychiatry and Behavioral Sciences,
Stanford University, Lab Surge Building, 1201 Welch Road, Room
P126, Palo Alto, CA 94304, USA
                                                                                                                                         Homo saptens chromosome
AF042305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 69), Lin,X., Voros,A., Underhill,P. and Mignot,E. Microsatellite single nucleotide polymorphisms in the HLA-DQ region Tissue Antigent 52 (1), 9-18 (1998) 98378271
Homo sapiens
Eukaryota; Metakoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primatęs; Catarrhini; Hominidae; Homo.

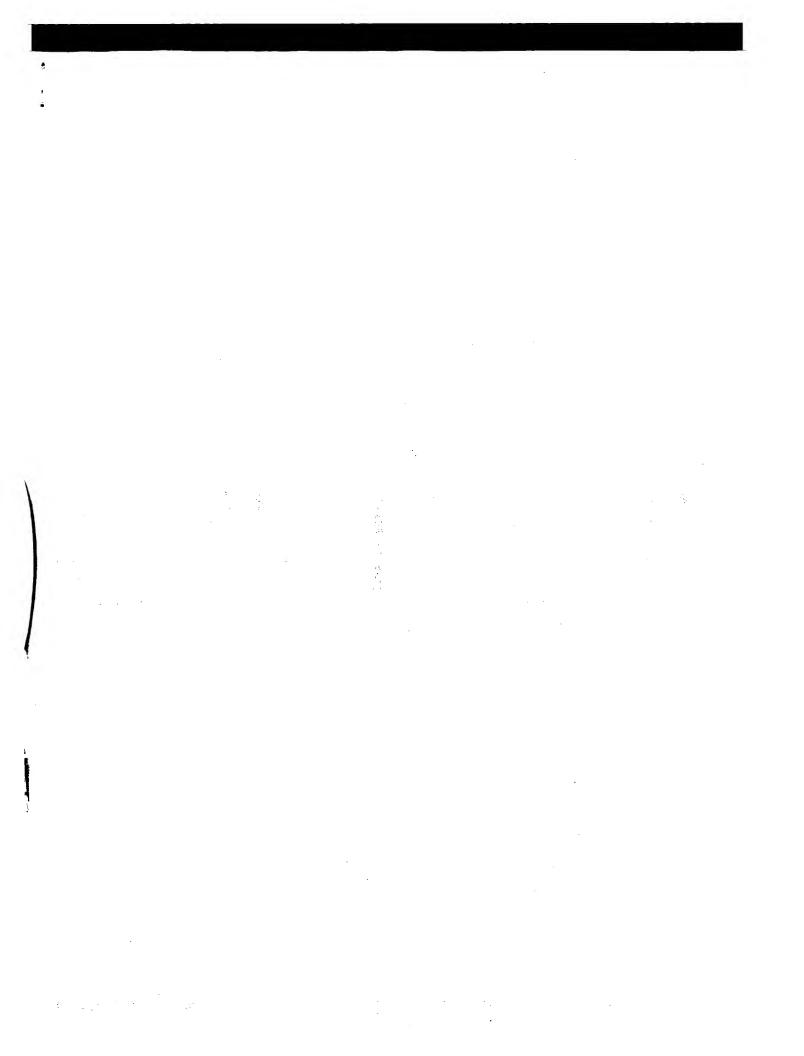
1 (bases 1 to 83)
Lin, L., Ain, L., Kanura, A., Carrington, M. and Mignot, E.
DO microsatellite association studies in three ethnic groups
Tissue Antigens 50 (5), 507-520 (1997)
98049194
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DQ microsatellite association studies in three ethnic groups
Tissue Antigns 50 (5), 507-520 (1997)
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1 (bases 1 to 69)
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/rpt_unit=ca
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Submitted (12-JAN-1998) Psychiatry and Behavioral Sciences,
Stanford University, Lab Surge Building, 1201 Welch Road, Room
P126, Palo Alto, CA 94304, USA
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Lin,L., Jin,L., Lin,X., Voros,A., Underhill,P. and Mignot,E.
Microsatellite single nucleotide polymorphisms in the HLA-DQ region
Tissue Antigens 52 (1), 9-18 (1998)
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Repeat sequence from polymorphic marker clone Mfd102.
Polymorphism; repeat sequence; genetic marker; primer; amplification;
PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
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pr d(G-dA)n(dG-dT)n - using novel nucleic acid mols. as primers

Claim 1; Column 13-14; 186pp; English.

PS Claim 1; Column 13-14; 186pp; English.

CC having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic

CC markers. Primers based on these sequences can be used to detect these

CC repeats, especially for use in e.g paternity or maternity testing,

CC human genetic analysis such as inhage analysis of genetic disease,

CC commercial animal or plant breeding or pedigree analysis. Clones

CC containing the repeat sequences were isolated by hybridisation of

CC chromosome-specific phage libraries with a synthetic poly(GC-dA).(dG-dT)

probe. Over 100 repeat blocks were isolated. The inserts from the clones

CC probe. Over 100 repeat blocks were isolated. The inserts from the clones

CC were amplified by primers T65798-T66047. Those clones where the repeat

Sequence has been determined are shown in T65704-797. This repeat

CC sequence having the formula: (AC)19AA(AC)5A.

Sequence 51 BP; 27 A; 24 C; 0 G; 0 U;
gene mapping, and selective breeding
Table 7; Page 301; 517pp; English.
The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine MboI DNA fragments of between
screening a library of bovine MboI DNA fragments of between
conclusion of the corosatellites and a (TC)15 oligonucleotide probe.
Cone out of 50 clones cross-hybridised. Assuming independent
distribution of microsatellites and MboI sites, the frequency of
(T6)n >9 microsatellites in the bovine genome is estimated at >100,
CON The sequence information for ca. 230 such bovine microsatellites
is summarised in the specification and indexed herein (see below).
The sequences upstream and downstream of the microsatellite sequence
were used to generate the required PCR primers for in vitro
applification of the corresp. microsatellite (using the program
optipram). The microsatellites may be used to identify individuals,
Cor parentage testing, and in the genetic mapping of economic trait
coloci, or genes involved the determinism of economically important
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US582979-A.
10-DEC-1996.
21-APR-1989; 341562.
21-APR-1989; US-341562.
05-SEP-1991; US-754351.
04-APR-1994; US-222177.
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Q33930;
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15-JAN-1992; U00340.
15-JAN-1991; US-642342.
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Microsatellite sequence from clone TGLA337.
PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
Bos taurus
Bos taurus
MO9213102-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENN-) GENMARK.
Georges M, Massey JM;
WPI; 92-284684/34.
Polymorphic bovine DNA markers - used in genetic identification,
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1 Similarity 100.0%;
38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          e analysis; genetic disease; isation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MARSHFIELD
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DT 02-F
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Q33828/C
ID Q338
AC Q338
AC Q338
DT Q2-E
DT M1CI
KW PCR;
KW PCR;
KW Gene
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PA (GERM) JGENARK.

PA (GERM) JGENARK.

DR WPI; 92-284684/34.

PT Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding gene mapping, and selective breeding property of the sequence 15 that of a bovine microsatellite sequence obtd. by CC Streening a library of bovine mbor DNA fragments of between CC one out of 50 clones cross-hybridised. Assuming independent CC distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, CC one in the sequence information for ca. 230 such bovine microsatellites compared to the sequence of in the specification and indexed herein (see below).

CC office sequences upstream and downstream of the microsatellite sequence ware used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program CC oppirrin). The microsatellites may be used to identify individuals, CC inci, or genes involved the determinism of economic trait craits esp. in cattle, to allow selective breeding.

Sequence 70 BP; 1 A; 1 C; 33 G; 35 T;
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Matches 37
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W09213102-A.

06-AUG-1992.

15-JAN-1992; U00340.

15-JAN-1991; US-642342.
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See also
Sequence
                                                                            02-EEB-1993 (first entry)
Microsatellite sequence from clone TGLA23.
PCR; selection; primers; OPTIRRIM; breeding; genetic mapping; traits; amplification; ss.
Bos taurus
MO9213102-A.
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Microsatellite sequence from clone TGLA26.
PCR; selection; primers; OPFIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                   Q33828 standard; DNA; 36 BP Q33828;
                06-AUG-1992.
15-JAN-1992; U00340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 Similarity
37; Conser
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l Similarity 100.0%;
37; Conservative (
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Pred. No
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Pred. No.
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0.0013;
                                                                                                                                                                                              cattle;
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CC The sequence is that of a bowlne microsatellite sequence obtd. by cc screening a library of bowlne microsatellite sequence occ 250 and 500 bp with an (AC)15 and a (TC)15 oligonucjectide probe. CC cone out of 50 clones cross-hybridised. Assuming independent cc distribution of microsatellites and MboI sites, the frequency of cc (T6)n >9 microsatellites in the bowlne genome is estimated at >100, cc is summarised in the specification and indexed herein (see below). CC The sequences upstream and downstream of the microsatellites commarised in the specification and indexed herein (see below). CC me used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program CC opTiPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait cc corresp. In cattle, to allow selective breeding.

See also Q33501-34437.

So Sequence 36 BP; O A; O C; 18 G; 18 T;
PA (GEMM-) GENMARK.

PA (GEMM-) GENMARK.

DR WPI; 92-284684/34.

DR WPI; 92-284684/34.

DR WPI; 92-284684/34.

PT polymorphic bovine DNA markers - used in genetic identification, properly gene mapping, and selective breeding rable 7; Page 282; 517pp; English.

CC The sequence is that of a bovine microsatellite sequence obtd. by compared the sequence of solution of microsatellites and Mbol Sites, the frequency of compared of the sequence of the bovine genome is estimated at >100, of the sequence information for ca. 230 such bovine microsatellites in the bovine denome is estimated at >100, of the sequence of the sequence of the microsatellites of the sequence of the sequence of the sequence of the microsatellites of the sequence of the microsatellites of the sequence of the microsatellite sequence of the sequence of the microsatellite (using the program of period of the corresp. microsatellite (using the program of control of the sequence of the microsatellite (using the program of the sequence of the microsatellite (using the program of control of the sequence of the sequence of the microsatellite (using the program of the sequence o
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Matches 36
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(GENM-) GENMARK.
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15-JAN-1991; US-642342.
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0; Mismatches
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0.0031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cattle; parentage;
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Q3393/c
ID 9339
AC Q339
AC Q33
RESULT
Q34041/
Q3401
ID 0340
AC Q340
AC Q340
AC Q340
PCR:
KW PCR:
KW PCR:
KW PCR:
KW Gene
OS Bos
PN W092
PD 06-A
PF 115-J
PR 115-J
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PI Georges M, Massey JM;

PT Polymorphic bovine DNA markers - used in genetic identification,

PT Polymorphic bovine DNA markers - used in genetic identification,

PT gene mapping, and selective breeding

PT gene mapping, and selective breeding

PT Table 7; Page 311; 517pp; English.

CC Table 7; Page 311; 517pp; English.

CC Table 7; Page 311; 517pp; English.

CC Screening a library of bovine MboI DNA fragments of between

CC 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.

CC 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.

CC One out of 50 clones cross-typbridised. Assuming independent

CC (T6)n >9 microsatellites in the bovine genome is estimated at >100,

CC (T6)n >9 microsatellites in the bovine genome is estimated at >100,

CC OND The sequence information for ca. 230 such bovine microsatellites

CC is summarised in the specification and indexed herein (see below).

CC The sequences upstream and downstream of the microsatellite sequence

CC were used to generate the required PCR primers for in vitro

CC amplification of the corresp. microsatellite (using the program

CC oppiprixib). The microsatellites may be used to identify individuals,

CC of the sequence in the program and in the meanting of economic traiting traits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                              WO9213102-A.
06-AUG-1992.
15-JAN-1992; U00340.
15-JAN-1991; US-642342.
(GENM-) GENMARK.
Georges M, Massey JM;
WPI; 92-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Microsatellite sequence from clone TGLA35. PCR; selection; primers; OPTIPRIM; breeding; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                     02-FEB-1993 (first entry)
02-FEB-1993 (first entry)
Microsatellite sequence from clone TGLA433.
PCR; selection; primers; OPTIPRIM; breeding;
genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also 033501-34437.

Seguence 36 BP; 0 A; 0 C; 18 G; 18 T;
                                                                                                                                                                                                                                                                                                                                      Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q34041 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JAN-1991; US-642342.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 CACACACACACACACACACACACACACACACACA 1
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    bovine DNA markers
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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    used in
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genetic identification
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pr gene mapping, and selective breeding
Table 7: Page 347: 517pp; English.

Che sequence is that of a bowine microsatellite sequence obtd. by
Cs creening a library of bowine MooI DNA fragments of between
Cs one out of 500 pb with an (AC)15 and a (TC)15 oligonucleotide probe.
Cc one out of 50 clones cross-hybridised. Assuming independent
Cc one out of 50 clones cross-hybridised. Assuming independent
Cc of the sequence information for ca. 230 such bowine microsatellites in the bowine genome is estimated at >100,
Cc of the sequence information for ca. 30 such bowine microsatellites
Cc is summarised in the specification and indexed herein (see below).
Cc the sequences upstream and downstream of the microsatellite sequence
Cc amplification of the corresp. microsatellite (using the program
Cc opTIPRIM). The microsatellites may be used to identify individuals,
Cc of arentage testing, and in the genetic mapping of economic trait
Cc loci, or genes involved the determinism of economically important
Cc traits esp. in cattle, to allow selective breeding.
See also 033501-34437.
See also 033501-34437.
See sequence 37 BP; 0 A; 0 C; 18 G; 19 T;
                                                                                                                                                 gene mapping, and selective breeding
Table 7: Page 402; 517pp; English.

CC The sequence is a boyine microsatellite sequence obtd. by
CS screening a library of boyine Morosatellite sequence of between
CS 30 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.
CC one out of 50 clones cross-hybridised. Assuming independent
CS of increased littles in the boyine genome is estimated at >100,
CC (Moin >9 microsatellites in the boyine genome is estimated at >100,
CC (Moin >9 microsatellites in the boyine genome is estimated at >100,
CC (Moin >9 microsatellites in the boyine genome is estimated at >100,
CC (Moin >9 microsatellites in the boyine genome is estimated at >100,
CC (Moin >9 microsatellites may be used howine microsatellites
CC (Moin >9 microsatellites microsatellite sequence
CC (Moin >9 microsatellite (Moint Moint Mo
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Best Local :
                                            Query Match
Best Local Similarity
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                Matches
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Georges M, Massey JM;
WPI; 92-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-FEB-1993 (first entry)
Microsatellite sequence from clone TGLA94.
PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q34178 standard; DNA; 37 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polymorphic bovine DNA markers - used in genetic identification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36
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                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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US-642342.
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0.1%; >cc
100.0%; Pr
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Pred. No. 0.0031;
                                            Score 36; DB 1;
Pred. No. 0.0031
                Mismatches
                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 37;
                                                                       Length 37;
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Best Local S
Matches 36
                                                                                                                                                                                                                                                    Homo sapiens.
US5582979-A.
                                                                                                                                                                                                                                                                                                             hybridisation;
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36; Conserv
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Length 37; Indels

0; Gaps

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RESULT 10
Q33900/C
ID Q33900
DT 02-FED
DE MICTOS
KW PCC; S
KW Geneti
PO 06-AUG
PD 15-JAN
PR 15-J
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                                                                                                                                                                                                                                             PA (GENM) GENNARK.

PA (GENM) GENNARK.

DR WPI: 92-284684/34.

DR WPI: 92-284684/34.

PI polymorphic bovine DNA markers - used in genetic identification, properly gene mapping, and selective breeding properly gene mapping, and selective breeding properly gene mapping, and selective breeding properly gene mapping, and selective broine microsatellite sequence obtd. by creaming a library of bovine mboi DNA fragments of between concept of 50 clones cross-hybridised. Assuming independent concept of 50 clones cross-hybridised. Assuming independent concept of microsatellites and Mboi sites, the frequency of concept of microsatellites and Mboi sites, the frequency of concept of microsatellites and Mboi sites, the frequency of concept of microsatellites and mboi sites, the frequency of concept of microsatellites and mboi sites, the frequency of concept of microsatellites and mboi sites, the frequency of concept of microsatellites and more sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below).

The sequences upstream and downstream of the microsatellite sequence concept in the corresp. microsatellite (using the program concept concept testing, and in the genetic mapping of economic trait concipt of genes involved the determinism of economically important concept concept concept of the cattle, to allow selective breeding.

Sequence 37 BP; 0 A; 0 C; 18 G; 19 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-FEB-1993 (first entry)
Microsatellite sequence from clone TGLA310.
PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-AUG-1992.
15-JAN-1992; U00340.
15-JAN-1991; US-642342.
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J. 0.0031;
O;
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10-DEC-1996:
21-APR-1989; 341562.
21-APR-1989; US-341562.
21-APR-1999; US-754351.
04-APR-1994; US-722177.
(MARS-) MARSHFIELD CLINIC.
Weber JL;
Weber JL;
WPI; 97-042299/04.
Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as
                                                                                                                                                                                                                                        T65732 standard; DNA; 37 BP.
T65732;
T165732;
T17-TUN-1997 (first entry)
T17-TUN-1997 (first entry)
Repeat sequence from polymorphic marker clone Mfd30.
Repeat sequence; genetic marker; primer; amplification;
Polymorphism; repeat sequence; genetic marker; primer; human; pedigree
PCR; polymerase chain reaction; paternity; maternity; human; pedigree
Linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                           chromosome;
      primers
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1 CACACACACACACACACACACACACACACACACACA 36

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PT (dC-dA)n(dG-dr)n - usiny nover nuclear (dC-dA)n(dG-dr)n (dG-dr)n (dG-dr)n (dG-dr)n which can be used as genetic CC The invention relates to the isolation of polymorphic repeat sequences CC The invention relates to the isolation of polymorphic repeat sequences CC markers. Primers based on these sequences can be used to detect these commarcial animal for use in e.g paternity or maternity testing, CC human genetic analysis such as linkage analysis of genetic disease, CC commercial animal or plant breeding or pedigree analysis.

CC The repeats, when analysed, fall into 4 categories:

CC The repeats which are alternating tandem CA repeats with no cc interruptions and without adjacent repeats of more runs of uninterrupted CC A repeats which are defined as 2 or more runs of uninterrupted CC 2) imperfect repeats which are defined as 2 or more runs of CA separated CC y interrupted dinucleotide or longer repeat bases from a run of at least CC uninterrupted dinucleotide or longer repeats of a sequence other than CC (dC-dA)n.(dG-dT)n, or from at least 10 uninterrupted mononucleotides; and CC ompound repeats except that the runs of CA are interrupted.
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PS Disclosure; Column 9-10; 186pp; English.

CC The invention relates to the isolation of polymorphic repeat sequences

CC having the sequence (dC-dA)n. (dG-dT)n which can be used as genetic

CC markers. Primers based on these sequences can be used to detect these

CC repeats, especially for use in e.g paternity or maternity testing,

CC human genetic analysis such as linkage analysis of genetic disease,

CC commercial animal or plant bereeding or pedigree analysis. Clones

CC containing the repeat sequences were isolated by hybridisation of

CC probe. Over 100 repeat blocks were isolated. The inserts from the clones

CC were amplified by primers 765798-766047. Those clones where the repeat

CC sequence has been determined are shown in 765704-797. This repeat

CC sequence is from the marker clone Mdf30 which contains the repeat

CC sequence as from the formula: (AC)185.

Sequence 37 BP; 19 A; 18 C; 0 G; 0 U;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                   Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers Example 8; Column 57-58; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-SEP-1991;
04-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Weber JL;
WPI; 97-042299/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (dC-dA)n.(dG-dT)n polymorphic repeat sequence #1.
Polymorphism; repeat sequence; genetic marker; primer; amplification;
PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MARS-) MARSHFIELD CLINIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66048 standard;
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36; Conser
                   e presented (AC)19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  341562.
; US-341562.
; US-754351.
; US-222177.
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 19
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                                       here
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                                     that the runs of CA here is an example of
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Pred. No.
 19
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0.0031;
<u>ن</u>
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                                       repeat sequence
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Query Match Best Local Similarity

0.1%;

Score 36; Pred. No.

DB 1; 0.003;

Length

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RESULT
T65750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DR WPI; 97-042299/04.

DR Detection of polymorphic genetic markers of the form PT (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers PT (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers PT (dC-dA)n(dG-dT)n + 1-12; 186pp; English.

PS Disclosure; Column 11-12; 186pp; English.

CC having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic CC markers. Primers based on these sequences can be used to detect these CC commercial primers based on these sequences can be used to detect these CC commercial animal or plant breeding or paternity or maternity testing, CC commercial animal or plant breeding or pedigree analysis of genetic disease, CC containing the repeat sequences were isolated by hybridisation of CC chromosome-specific phage libraries with a synthetic poly(dC-dA).(dG-dT) CC corosome-specific phage libraries with a synthetic poly(dC-dA).(dG-dT) CC corosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) CC corosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) CC corosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) CC corosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) CC corosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) CC corosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) CC sequence has been determined are shown in T65704-797. This repeat CC sequence is from the marker clone Mdf50 which contains the repeat CC sequence 38 BP; 19 A; 19 C; 0 G; 0 U;
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                 Georges M, Massey JM;
WPI; 92-284684/34
                                                                                     06-AUG-1992.
15-JAN-1992; U00340.
15-JAN-1991; US-642342.
                                                                                                                                                             genetic mapping;
Bos taurus.
                                                                                                                                                                                            Microsatellite sequence f
PCR; selection; primers;
                                                                                                                                                                                                                                                    Q33648 standard; DNA; 39
Q33648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-APR-1989; 341562.
21-APR-1989; US-341562.
05-SEP-1991; US-754351.
04-APR-1994; US-222177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Repeat sequence from polymorphic marker clone Mfd50.
Polymorphism; repeat sequence; genetic marker; primer; amplification;
PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
linkage analysis; genetic disease; animal; plant; breeding; locus;
Polymorphic bovine DNA markers - used gene mapping, and selective breeding
                                                                                                                                            WO9213102-A.
                                                                                                                                                                                                                                   02-FEB-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hybridisation; chromosome; ds.
                                                                      (GENM-) GENMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MARS-) MARSHFIELD
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                                                                                                                                                                                                                                                                                                                                                           0.1%;
l Similarity 100.0%
36; Conservative
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                                                                                                                                                                                                                                 (first entry)
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0;
                                                                                                                                                                                          from clone MTGT4B.
; OPTIPRIM; breeding;
                                                                                                                                                                                                                                                                      ВP
                                                                                                                                                                             amplification; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36; DB
Pred. No. 0.0
0; Mismatches
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                  in genetic identification,
                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
0.003;
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                                                                                                                                                                                                cattle;
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 x_0

Table 7; Page 189; 517pp; English.

The sequence is that of a bovine microsatellite sequence obtd. by creening a library of bovine mbor DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.

Cone out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbor sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, clones from the bovine genome is estimated at >100, clones from the sequence information for ca. 20 such bovine microsatellites is summarised in the specification and indexed herein (see below).

The sequences upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program of the microsatellites and the specific mapping of economic trait of premers for in vitro appropriate testing, and in the genetic mapping of economic trait traits esp. in cattle, to allow selective breeding.

See also 033501-34437.

Sequence 39 BP; 0 A; 0 C; 19 G; 20 T;

Query Match 0.1%; Score 36; DB 1; La Best Local Similarity 100.0%; Pred. No. 0.003; Matches 36; Conservative 0; Mismatches 0;

Length 39; Indels

0

Gaps

0

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RESULT 13807/C 033807/C 1D 033807/C 1D 0338 AND 0238 AND 
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                                                                                                                                                                                                                                                                                                                                     gene mapping, and selective breeding general appling and selective breeding general appling, and selective breeding. The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between cone out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, cone out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, cone out of 50 clones cross-hybridised. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellites expenses the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program opripring). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait traits esp. in cattle, to allow selective breeding. See also 033501-34437.

See also 033501-34437.

Sequence 39 BP: 0 A; 0 C; 20 G; 19 T;
                                                                                                                                    Query Match
Best Local Similarity
Matches 36; Conserv
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Microsatellite sequence from clone TGLA213.
Microsatellite sequence from clone TGLA213.
PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
Bos taurus.
MC9211102-A.
MC9211102-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Georges M, Massey JM;
WPI; 92-284684/34.
Polymorphic bovine DNA markers - used in genetic identification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-AUG-1992.
15-JAN-1992; U00340.
15-JAN-1991; US-642342.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15
ch 0.1%; Score 36; DB 1 Similarity 100.0%; Pred. No. 0.0 36; Conservative 0; Mismatches
                                                                                                                                                                            Score 36; DB 1;
Pred. No. 0.003;
                                                                                                                                         0,
                                                                                                                                                                                                                     Length 39
                                                                                                                                         Indels
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                                                                                                                                    Gaps
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밁 39 CACACACACACACACACACACACACACACACACA

Search completed: March 29, 2000, 13:08:06 Job time: 33484 sec

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Title:
Perfect score:
Sequence:
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Maximum DB seq length: 105
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Copyright (c) 1993 - 2000 Compugen Ltd.
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SUMMARIES

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ACCESSION

G31304 96 bp DNA STS 29-SEP-1998 \$y89991-19 Human (A.Gnirke) Homo sapiens STS genomic, sequence tagged site. G31304

ALIGNMENTS

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BASE COUNT
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Matches 89; Conservative 0; Mismatches 0; Indels
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131237 56 bp DNA
Sequence 149 from patent US 5582979.
131237
131237.1 GI:1822028
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GDB_DSGG: D652377
Contact: Andreas Gnirke
Mercator Genetics, Inc.
4040 Campbell ave, Menio Park CA, 94025, USA
Email: gnirke@mercator.com
Primer A: GTCCCCAPAGRATATAAATGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 96)

Lauer, P., Meyer, N.C., Prass, C.E., Starnes, S.M., Wolff, R.K. and
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Genome Res. 7 (5), 457-470 (1997)
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STS size: 77
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PCR Cycles:
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/db_xref="taxon:9606"
/clone_lib="Human (A.Gnirke)"
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10 mM
8.3
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each 200 uM
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60 degrees C for 45 seconds
72 degrees C for 60 seconds
35
MJ Research PTC-200
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Homo sapiens DNA.

Homo sapiens DNA.

Homo sapiens Eukaryota, Metazoa: Chordata; Craniata; Vertebrata; Mammalia; Eukaryota, Metazoa: Chordata; Craniata; Hominidae; Homo.

1 (bases 1 to 85)

2 (Characterization and purification of HITF2, a novel CCAAT-binding protein that interacts with a histone H1 subtype-specific consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unclassified.
1 (bases 1 to 56)
Weber, J.L.
                                                                                                                                                                                                                                                                                                      On Jul 23, 1994 this sequence version replaced gi:341438 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                 Mol. Cell. Biol. 9 (4), 1566-1575 (1989)
89261784
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Homo sapiens histone 1 gene, promoter region.
M26162
M26162.1 GI:514937
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53. .85
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/db_xref="taxon:9606"
/cell_line="HeLa"
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                                                   0.2%; Score 46; DB 10;
100.0%; Pred. No. 3.2e-12;
Live 0; Mismatches 0;
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AR002288

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HUMUT578A
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Human STS UT578, 5' pi
L39139 L18336
L39139.1 GI:642101
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Sequence
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Orr,H.T., Ranum,L.P.W., Chung,M. and Zoghbi,H.Y.
Gene sequence for spinocerebellar ataxia type 1 and method
                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 54)
Orr,H.T., Ranum,L.P.W., Chung,M. and Zoghbi,H.Y.
Gene sequence for spinocerebellar ataxia type 1
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 69)
Gerken,S.C., Matsunami,N., Plaetke,R., Albertsen,H., Ballard,
                                              Homo sapiens
                                                                    STS; PCR primer; STS sequence; microsatellite DNA; microsatellite marker; sequence tagged site; tetranucleotide repeat.
                                                                                                                                                                                                                                                                                                                                                           Patent:
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                                                          Homo sapiens DNA.
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Location/Qualifiers
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J. 1.1e-10;
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1.1e-10;
hes 0; Indels
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10109 TTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAA 10150
                  8640 TCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 TTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAA 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genetic and physical mapping of simple sequence reg sequence tagged sites from the human genome uppublished (1994)
Submitted by: Utah Center for Human Genome Research Utah, Dept. of Human Genetics 2160 Eccles Institute of Human Genetics 2161 Eccles Institute of Human Genetics Salt Lake City, UT 84112
e-mail: sts@corona.med.utah.edu
Primer A: AGGTGGAGACCAGCCTGGC
Primer B: AGGTGGAGAAATCGCATC
End to Label: Primer A
PCR Profile:
TCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Initial Denaturation: 94C 300sec Cycles Denaturation Annealing C 10 sec. 62 C 10 sec. 72 C 20 sec. 58 C 10 sec. 72 C 20 sec. Mg++: 1.50 Gel: Acrylamide 7%, Formamide 32%, Urea 34% Alleles: 1.
                                                                                                                                                                                                                                                                                         1 (bases 1 to 40)
Resnick M.A., Larionov, V.L., Kouprina, N.Y. and Perkins, E.L.
TRANSFORMATION-ASSOCIATED RECOMBINATION CLONING
Patent: wo 9801573-A 15-JAN-1998;
US HEALTH (US)
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Sequence 1 from
A68621
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Robertson,M., Bradley,P., Elsner,T., Tingey,A., Lalouel,J.-M. and
White,R.
                                                                                                                                                                                                                                                                                                                                                                                               unclassified
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/db_xref="taxon:9606"
/map="19"
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16 c 14 g
                                                                                                                                                                                              /db_xref="taxon:32644"
12 c 13 g
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n Patent WO9801573.
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; Pred. No. 3.7e-10;
0; Mismatches 0;
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                                                                                             Score 40; DB 5; L
Pred. No. 4.1e-09;
                                                                            Mismatches
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LOCUS DEFINITION ACCESSION

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TITLE JOURNAL MEDLINE REMARK

SOURCE ORGANISM

KEYWORDS

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Ouery Match 0.2%; Score 40; DB 10; Length 101; Best Local Similarity 100.0%; Pred. No. 4e-09; Matches 40; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               $79561 101 bp DNA PRI 27-7AN-1996 dHRX [partial genomic duplication startpoint] [human, acute myeloid leukemia with trisomy 11 syndrome patient J, Genomic Mutant, 101
                                                                                                                                          GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 179936] from the original journal article. This sequence comes from Fig. 3.
Map location: 11q23.
                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 101)

Bernard, O.A., Romana, S.P., Schichman, S.A., Mauchauffe, M.,
Jonveaux, P. and Berger, R.
Partial duplication of Hrx in acute leukemia with trisomy 11

Leukemia 9 (9), 1487-1490 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 170933] from the original journal article. This sequence comes from Fig. 3.
Map location: 11q23.
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1 (bases 1 to 101)

Bernard,O.A., Romania,S.P., Schichman,S.A., Mauchauffe,M.,
Jonveaux,P. and Berger,R.
Partial duplication of HRX in acute leukemia with trisomy 11
Leukemia 9 (9), 1487-1490 (1995)

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HRX (Intron 6) [human, Genomic, 101 nt].
$79560
$79560.1 GI:1168041
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Location/Qualifiers
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                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
  /gene="dHRX"
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I31174/c
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Matches 39; Conserv
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Sequence 86 from patent US 5582979.
I31174 GI:1821965
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                                                                                                                                                                                                              Patent: US 5712098-A 1 27-JAN-1998;
Location/Qualifiers
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                                                                                                                                                                                                                                                                                      Unclassified.
                                                                                                                                                                                                                                                                                                                                                                            Unknown.
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Sequence 1 from patent US
182155
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method of using the same
Patent: US 5582979 A 86 10-DEC-1996;
Location/Qualifiers
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                                                 0.2%; Score 39; DB 5; Lotarity 100.0%; Pred. No. 1.3e-08; Conservative 0; Mismatches 0;
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8 c 15 g
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RESULT S79561 LOCUS

DEFINITION

SOURCE ORGANISM KEYWORDS

ACCESSION VERSION

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AUTHORS

JOURNAL MEDLINE REMARK

TITLE

BASE COUNT ORIGIN

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FEATURES

COMMENT FEATURES

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Homo sapiens
AF042304
                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovicaprine; Ovis.

1 (bases 1 to 102)

Crawford, A.M. and Buchanan, F.C.

Ovine dinucleotide repeat polymorphisms at the FCB11, FCB128, FCB193, FCB566 and FCB304 loci
                                                                                                                                             Ovis aries DNA.
                                                                                                                                                                                                          Sheep dinucleotide repeat polymorphism at
                                                                                                                                                                    dinucleotide repeat polymorphism
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                                                                                                                                                                                    L01534.1 GI:165865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 75)
Lin,L., Jin,L., Kimura,A., Carrington,M. and Mignot,E.
DQ microsatellite association studies in three ethnic groups
Tissue Antigens 50 (5), 507-520 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF042304.1
STS.
                                         Unpublished (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lin,L., Jin,L., L:
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lin,L., Jin,L., Lin,X., Voros,A., Underhill,P. Microsatellite single nucleotide polymorphisms Tissue Antigens 52 (1), 9-18 (1998) 98378271
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    1. .102
/organism="Ovis aries"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="microsatellite"
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the FCB266 locus.
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ch 0.2%; Score 38; DB 5; I
1 Similarity 100.0%; Pred. No. 4.3e-08;
38; Conservative 0; Mismatches 0;
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Sequence
AR002290
                                                                                                                                         1 (bases 1 to 66)
Orr,H.T., Ranum,L.P.W., Chung,M. and zoghbi,H.Y.
Gene sequence for spinocerebellar ataxia type 1
diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
AR051487
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1 (bases 1 to 60)

de la Monte, S. and Wands, J.R.

Neural thread protein gene expression
                                                                                                                               Patent:
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/cell_type="leukocyte"
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                                                                           /organism="unknown"
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Page 6

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                STS 29-SEP-1998
STS genomic, sequence
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G31304 sy899g1-19
AF062763 Glycine m
G37948 C4M78 Plasm
G37948 C4M78 Plasm
G37948 C4M78 Plasm
M15365 Human low d
L36843 Homo sapien
M15365 Human low d
AF062763 Glycine m
M87899 Human carci
I82155 Sequence 1
I88893 Sequence 1
I88893 Sequence 1
M36131 Human alpha
A68622 Sequence 2
AR063068 Sequence 2
AR063068 Sequence 3
AR063068 Sequence 1
A9118 Sequence 13
A49118 Sequence 13
A49118 Sequence 19

Description

AR001312 Sequence

K03555 Human low d
129931 Sequence 4

A48799 Sequence 6
136502 Sequence 1
129928 Sequence 7
189944 Sequence 7
189944 Sequence 7
189948 Sequence 7
189949 Sequence 8
189515 H.sapiens (
A08907 H.sapiens (
A08908 Frobe. 6/19
E12579 Probe. 6/19
E12580 Probe. 6/19
E12580 Probe. 6/19
E12580 Probe. 6/19
E13630 Probe. 6/19
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E17120 DNA Probe.
M25215 Dictyostel1
A08909 H.sapiens (
149625 Sequence
A08911 H.sapiens (
A08911 H.sapiens (
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MEDLINE
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                                                                                                                931 TCTGCCCCTCTTCCCACTGTGCCCTGGGG 959
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Andreas Gnirke
Mercator Genetics, Inc.
4040 Campbell Ave, Menlo Park CA, 94
Email: gnirke@mercator.com
Primer B: AGGCACAAGAATATAAATGAG
Primer B: AGGCACAGTGGGAAG
STS Size: 77
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G31304.1
STS.
AF062763 92 bp DNA
Glycine max microsatellite AF062763
AF062763.1 GI:3372757
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GDB_DSEG: D6S2377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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KC1: 50 mM

Tris-HC1: 10 mM

pH: 8.3

gelatin: 0.001% (W/V).

Location/Qualifiers
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1 29 c 23 g
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/db_xref="taxon:9606"
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AUTHORS
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                                                                                            Bldg. 4, Room 126, NIH Campus, Be rat: (301) 496-4021
Fax: (301) 402-0079
Email: tew@helix.nih.gov
Primer A: GGAAATATACACAAAGCAATC
Primer B: AATTTACTTCCTGCATTTTCC
STS size: 99
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peakall, R., Gilmore, S., Keys, W., Morgante, M. and Rafalski, A. Cross-species amplification of soybean (Glycine max) simple-sequence-repeats (SSRs) within the genus and other legume genera: implications for the transferability of SSRs in plants peakall. Evol. (1998) In press (bases 1 to 92) Peakall, R., Gilmore, S., Keys, W., Morgante, M. and Rafalski, A. Direct Submission Submitted (04-MAY-1998) Division of Botany and Zoology, Australian National University, Canberra, ACT 0200, Australia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       soybean.
Glycine max
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
Machine:
Protocol:
                                                                                                                                                                                                                                                                                                                                    Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 99)
Su,X-z., Ferdig,M.T. and Wellems,T.E.
Integrated genetic and physical maps of Plasmodium falciparum
Unpublished (1998)
On Mar 6, 1999 this sequence version replaced gi:3056692.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      037948 99 bp DNA STS 26-FEB-1999 C4M78 Plasmodium falciparum haploid Plasmodium falciparum STS genomic, sequence tagged site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G37948.2 GI:4337425
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Peakall, R., Gilmor
                                                         Initial heat:
Cycles:
                                                                                                                                                                                                                                                                                               Contact: Thomas E. Wellems
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               malaria parasite P. falciparum.
                                                                                                                                                                                                                                                            NIAID
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/db_xref="taxon:3847"
5. .57
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                  2min at 94oC
30 cycles, each having steps 20sec at 94oC;
10sec at 45oC; 10sec at 40oC; 30sec at 60oC
Perkin Elmer GeneAmp 9600
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io. 1.5e-12; Indels
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G37948
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Integrated genetic and physical maps of Plasmodium falciparum
Unpublished (1998)
On Mar 6, 1999 this sequence version replaced gi:3056692.
                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1. (bases 1 to 99)
                                                                                                                                                                                            Tel: (301) 496-4021
Fax: (301) 402-0079
Email: tew@helix nih.gov
Primer A: GGAANTATACACAAGCAATC
Primer B: AATTTACTTCCTGCATTTTCC
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                                                                                  Protocol:
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                                                                                                                                                                                                                                                                               4, Room 126, NIH Campus, Bethesda, MD 20892-0425
dNTPs:
Taq Polymerase:
Total Volume:
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Total Volume:
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/dev_stage="erythrocytic haploid stage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Plasmodium falciparum"
/strain="HB3xDd2"
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                                                                                    2min at 94oC
30 cycles, each having steps 20sec at 94oC;
10sec at 45oC; 10sec at 40oC; 30sec at 60oC
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5 pM each
0.3 ul of 1
0.5 unit
15 ul
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 90)
Lehrman, M.A., Goldstein, J.L., Russell, D.W. and Brown, M.S.
Duplication of seven exons in LDL receptor gene caused by Alu-Alu recombination in a subject with familial hypercholesterolemia Cell 48 (5), 827-835 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 0.1%; l similarity 100.0%; 44; Conservative (
                                                                                                                                                                                                                                                                                                                               Clean copy of sequence kindly provided by M.Lehrman (22-APR-1987). Individual FH 295 carries two mutant LDL receptor alleles. The allele below was inherited from the father and includes a duplication of exons 2 through 8 that was presumably created by unequal chromosomal crossover involving Alu repeats in introns 1 and 8. The exact site of recombination cannot be determined because the sequences of the Alu repeats in introns 1 and 8 of normal alleles are identical over a span of 26 nucleotides at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Human low density lipoprotein receptor mutant gene recombination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     recombination.
Human (FH 295) fibroblast DNA, clone p295
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                                                                                                                                                                                                                                                                                                                   recombination site.
   đđ
   upstream
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1.5 mM MgCl2
50 mM KCl.
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/dev_stage="erythrocytic haploid stage"
1, .99
1, .20
//note-"LDLR duplicated intron 1 (no splice of 68); putative; does not fit consensus" 3 c 19 g 20 t cream of NheI site; chromosome 19p13.2-p13.1.
                                                                           /organism-"Homo sapiens" 68. .>90
                                                                                                                                                                       /gene="LDLR"
<1. .43
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6 c 10 g
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/db_xref="taxon:9606"
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                                                                                                                              /note="LDLR intron 8; G00-119-362"
                                                                                                                                                    'gene="LDLR"
                                                                                                                                                                                                                         /map="19p13.3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LDL receptor; cell surface protein; crossover;
                                                                                                                 . 68
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0. 1.7e-11;
ches 0;
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Matches 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                     1 Similarity
42; Conserv
Clean copy of sequence kindly provided by M.Lehrman (22-APR-198: Individual FH 295 carries two mutant LDL receptor alleles. The allele below was inherited from the father and includes a duplication of exons 2 through 8 that was presumably created by
                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 90)

1 (chases 1 to 90)

1 (chrman, M.A., Goldstein, J.L., Russell, D.W. and Brown, M.S.

1 Duplication of seven exons in LDL receptor gene caused by Alu-Alu recombination in a subject with familial hypercholesterolemia (cell 48 (5), 827-835 (1987)
                                                                                                                                                                                                                                                                                 HUMLDLRM 90 bp DNA PRI 11-JAN-1995 Human low density lipoprotein receptor mutant gene recombination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 89184542
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Homo sapie
                                                                                                                                                                               recombination.
Human (FH 295) fibroblast DNA, clone p295.
                                                                                                                                                                                                                      M15365.1 GI:187107
Alu repeat; LDL rec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ancient DNA: extraction, characterization, molecular cloning, enzymatic amplification
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L36843
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                                                                                                                                                                                                                                                                                                                                                                                                                                   0.1%; Score 42; DB llarity 100.0%; Pred. No. 1.9 Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="Alu"
18 c 23 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism-"Homo sapiens"
/isolate-"4000 year old :
/db_xref-"taxon:9606"
/tissue_type-"liver"
<1. .>67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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year old remains from Nekht-ankh
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                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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1 Alu repeat
                                          (22-APR-1987)
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AF062763/c
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             Query Match 0.1%; Sometime 0.1%; Sometime 0; Matches 41; Conservative 0;
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                 Score 41; DB; Pred. No. 6.0
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DB 8; Le.. 5. 6.3e-10; 0;

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Db 78 GIGGTCATGCCTGTAATCCCAGCACTTTGGGAGGCTGAGG 23633
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                                                                                                                                                                                                                                                              Direct Submission
Submitted (04-MAY-1998) Division of Botany and Zoology, Australian
National University, Canberra, ACT 0200, Australia
                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 92)

PeakAll,R., Gilmore,S., Keys,W., Morgante,M. and Rafalski,A.

Peaksall,R., Gilmore,S., Keys,W., Morgante,M. and Rafalski,A.

Cross-species amplification of soybean (Glycine max)

Simple-sequence-repeats (SSRs) within the genus and other legume genera: implications for the transferability of SSRs in plants Mol. Biol. Evol. (1998) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arvoz/63 92 bp DNA PLN
Glycine max microsatellite AC21 repeat region.
AF062763
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Peakall,R., Gilmore,S., Keys,W., Morgante,M. and Rafalski,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytas; Spermatophyta; Magnollophyta; eudicotyledona; core
eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="LDLR duplicated intron 1 (no splice consensus at 68); putative; does not fit consensus"
18 a 33 c 19 g 20 t
upstream of NheI site; chromosome 19p13.2-p13.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.1%; Score 41; DB 9; L larity 100.0%; Pred. No. 6.3e-10; Conservative 0; Mismatches 0;
                                                                                                                 /organism="Glycine max"
/db_xref="taxon:3847"
6. .57
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   /rpt_type=tandem
/rpt_unit-ta
5 c 4
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/db_xref="taxon:9606"
/map="19p13.3"
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                                                                                         /note="microsatellite AC21"
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HUMALCE272/c
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             39
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 104)
Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.
Alu RNA transcripts in human embryonal carcinoma cells. Model post-transcriptional selection of master sequences
J. Mol. Biol. (1992) In press
J. Mol. Biol. (1992) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens male embryo carcinoma cDNA to other RNA Homo sapiens
                                                                                                                                                                                                                                                                                                                                                   Sequence 1 from pate
182155
182155.1 GI:3210452
                                                                                                                                                                                         Patent: US 5712098-A 1 27-JAN-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                  1 (bases 1 to 39)
Tsuchihashi, Z., Gnirke,
Wolff, R.K. and Feder, J
                                                                                                                                                                                                                                                                                                           Unknown
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M87899
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                                                                                                                                                                                                                                                                                                                        Unknown.
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                                                                0.1%; Score 39; llarity 100.0%; Pred. No. Conservative 0; Mismatc
                                                                                                                                                  /organism~"unknown"
8 c 15 g
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26 c 37 g 1
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/db_xref="taxon:9606"
/cell_line="NTera2D1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="male"
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na cell-derived Alu RNA transcript,
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m patent
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US 5712098
                                                                 Mismatches
                                                           DB 5;
5. 7.1e-09;
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HUMBRKFAA
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Sequence 2 from Patent WO9801573.
A68622
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                                                                                                                                                                  . Similarity 39; Conserv
                                                                                                                                                                                                                                                                                                                                                              Kornreich,R., Bishop,D.F. and Desnick,R.J. Alpha-galactosidase A gene rearrangements causing Fabry disease: Identification of short direct repeats at breakpoints in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fabry disease; breakpoint junction; glycosphingolipid catabolism \operatorname{\mathtt{Human}} DNA.
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Human alpha-galactosidase breakpoint region
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39; Conserv
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Suzuki,F., Hiraki,Y., Takahashi,K., Suzuki,J., Kondo,J., Kohara,A.,
Mori,A. and Yamada,E.
Human chondromodulin-I protein
Patent: US 5719125-A 11 17-FEB-1998;
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                                                                                                                                                                                                                                                                                                                          90264427
                                                                                                                                                                                                                                                                                                                                   Alu-rich gene
J. Biol. Chem. 265, 9319-9326 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                               0.1%; Score 39; DB llarity 100.0%; Pred. No. 7.: Conservative 0; Mismatches
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                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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8 c 8 g
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GI:4759649
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l Similarity 100.0%; Pred. No. 2.4e-08;
38; Conservative 0; Mismatches 0;
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Sequence 42 from patent US 5844075.
AR063068
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1 (bases 1 to 40)

1 (bases 1 to 40)

Resnick, M. A., Larionov, V.L., Kouprina, N.Y. and Perkins, E.L.

TRANSFORMATION-ASSOCIATED RECOMBINATION CLONING

Patent: WO 9801573-A 15-JAN-1998;
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 62)
Fleming, J.C., Pahl, H.L., Gonzalez, D.A., Smith, T.F. and Tenen, D.G. Structural analysis of the CD11b gene and phylogenetic analysis of
                                                                                                                                                                            S52152S31 62 bp DNA PRI 08-MAY-1993 CD11b-leukocyte integrin alpha chain [human, Genomic, 62 nt, segment 31 of 31].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unclassified.

1 (bases 1 to 58)

1 (kayakami,Y. and Rosenberg,S.A.

Melanoma antigens and their use in diagnostic and therapeutic
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                                                                                                                                                 $52228
$52228.1 GI:263048
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/db_xref="taxon:32644"
8 c 19 g
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BASE COUNT
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MEDLINE
REMARK
                                                           Query Match
Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                evolution J. Immunol 93123748
                                                                                                                                                                                                                              GenBank staff at the National Library of Medicine created this entry (NCBI gibbsq 121959) from the original journal article. This sequence comes from Fig. 3.

Map location: 16.
                                                                                                                                                                                                                                                                                                                                           the alpha-integrin gene family demonstrate remarkable conservation of genomic organization and suggest early diversification during
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                                                             Conservative
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/db_xref="taxon:9606"
2 c 1 g
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100.0%; Pred. No.
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Search completed: March 30, 2000, 00:22:34
Job time: 75503 sec

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Result
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Maximum DB
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Perfect score:
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      Issued_Patents_NA:*

1: /cgn2_6/ptodata/

2: /cgn2_6/ptodata/

3: /cgn2_6/ptodata/

4: /cgn2_6/ptodata/
5: /cgn2_6/ptodata/
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7: /cgn2_6/ptodata/
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length: 105
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Gapop 60.0 , Gapext 60.0
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10576.873 Million cell updates/sec
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                                           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/5C_COMB.seq:*
/cgn2_6/ptodata/1/ina/5D_COMB.seq:*
/cgn2_6/ptodata/1/ina/6_COMB.seq:*
/cgn2_6/ptodata/1/ina/6_COMB.seq:*
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US-08-222-177A-325
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US-08-222-177A-400
US-08-222-177A-400
US-08-222-177A-139
US-08-222-177A-183
US-08-222-177A-183
US-08-222-177A-232
US-08-222-177A-388
US-08-222-177A-388
US-08-222-177A-195
US-08-222-177A-195
US-08-222-177A-191
US-08-222-177A-101
US-08-222-177A-361
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                  325, App
140, App
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240, App
253, App
254, App
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256, App
257, App
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US-08-222-177A-249
                                                                US-08-222-177A-249
    Query Match
                                                                                                                                          TOPOLOGY:
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Sequence 421, App	Sequence 134, App		Patent No. 5506118	Sequence 244, App	Sequence 382, App	Sequence 128, App	Sequence 394, App	Sequence 307, App	Sequence 65, Appl	Sequence 304, App	Sequence 391, App	Sequence 337, App	Sequence 317, App	Sequence 89, Appl	Sequence 379, App	Sequence 367, App	Sequence 328, App	Sequence 186, App

ALIGNMENTS

SAME

Sequence 249, Application US/08222177A Patent No. 5582979 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/341,562 FILING DATE: 21-APR-1989 ATTORNEY/AGENT INFORMATION: NAME: Sara, Charles S. REGISTRATION NUMBER: 30,492 REFERENCE/DOCRET NUMBER: 09865.601 TELECOMMUNICATION INFORMATION: TELEPHONE: (608) 831-2100 GENERAL INFORMATION: APPLICANT: Weber, James L. TITLE OF INVENTION: LENGTH POLYMORPHISMS IN TITLE OF INVENTION: (dC_dA)n.(dG-dT)n SEQUENCES INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS MOLECULE TYPE: DI IMMEDIATE SOURCE: mfd69rs SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES: TYPE: nucleic acid TELEFAX: (608) 831-2106 APPLICATION NUMBER: FILING DATE: 53717-1914 Wisconsin DeWitt Ross & Stevens, S.C. 8000 Excelsior Drive, Suite 401 linear DNA (genomic) 460 US/08/222,177A 249: 09865.601 #1.25 AND METHODS ဝူ USING

0.18;

Score 38;

DB 1;

Length

44;

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RESULT 2
US-08-222-177A-325
; Sequence 325, App
US-08-222-177A-140
Sequence 140, Application US/08222177A
Sequence 140, Application US/08222177A
PATENT NO. 5582979
GENERAL INFORMATION:
APPLICANT Weber, James L.
APPLICANT WEBER OF INVENTION: (dC-da)n.(dG-d'
TITLE OF INVENTION: (dC-da)n.(dG-d'
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US-08-222-177A-325
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PATENT NO. 5582979

PATENTAL INFORMATION: James L.

APPLICANT: Weber, James L.

TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
TITLE OF INVENTION: (460 d)n. (dG-dT)n SEQUENCES AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 460

CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
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FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
APPLICATION NUMBER: US 07/341,562
APPLICATION NUMBER: 1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 09865.601
TELEPHONE: (608) 831-2100
TELEPHONE: (608) 831-2106
TELEPHAX: (608) 831-2106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 51 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Madison
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5582979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
LENGTH POLYMORPHISMS IN (dC-da)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/08/222,177A
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TOPOLOGY: linear
MOLECULE TYPE: DNA
MEDIATE SOURCE:
CLONE: mfd30rs
US-08-222-177A-140
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US-08-222-177A-198
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Best Local S
Matches 36
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MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:

COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNUMBER: US/08/222,177A
FILING DATE: CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 30,492
REGISTRATION UNUMBER: 09865.601
TELEPHONE: (608) 831-2106
TELEPAX: (608) 831-2106
                                                                                                                                                                                                                                                                                              Sequence 198, Application US/08222177A
Fatent No. 5582979
GENERAL INFORMATION:
APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 460
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 base pairs
TYPE: nucleic acid
ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,177A
FILING DATE:
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STREET: 80
CITY: Madi
                                                                                                                                                                       ADDRESSEE: DeWitt Ross & Stevens, S.C. STREET: 8000 Excelsior Drive, Suite 401 CITY: Madison STATE: Wisconsin COUNTRY: USA ZIP: 53717-1914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Madison
STATE: Wisconsin
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ZIP: 53717-1914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.1%; Score 36; DB 1; L
100.0%; Pred. No. 0.00085;
htive 0; Mismatches 0;
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 21-APR-1989

07/341,562

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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs

LENGTH: 100 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 397, Application US/08222177A Patent No. 5582979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local 9
                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 0988
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
TELEFAX: (608) 831-2106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                        ZIP: 53717-1914

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
             SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Weber, James L.
TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: GRANTSON THE CONS
                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 Similarity 100.0%;
36; Conservative 0
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                        Wisconsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: DeWitt Ross & Stevens, S.C.
8000 Excelsior Drive, Suite 401
                                                                             (808)
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                                                                                              608) 831-2100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    double
                                                                             831-2106
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Pred. No.
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RESULT

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; STRANDEDNESS:
; TOPOLOGY: line
; MOLECULE TYPE: I
US-08-222-177A-397
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                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 137, Application US/08222177A Patent No. 5582979
GENERAL INFORMATION:
APPLICANT: Weber, James L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local 9
                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 0949
REFERENCE/DOCKET NUMBER: 0986
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-216
                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 39 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 53717-1914

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                       IMMEDIATE SOURCE: CLONE: mfd29rs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Weber, James L.
TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                  STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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                             1 CACACACACACACACACACACACACACACACACA 36
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 2 CACACACACACACACACACACACACACACACA 37
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36; Conserv
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                                                                                                                                                                                                                                  nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wisconsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: DeWitt Ross & Stevens, S.C.
8000 Excelsior Drive, Suite 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                (608) 831-2100
(608) 831-2106
                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           double
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                                                                            100.0%;
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100.0%; Pred. No.
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                                                                              Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                09865.601
                                                             Mismatches
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                                                                              DB 1; L
                                                                                         Length 39;
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                                                             Gaps
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RESULT 8
US-08-222-177A-400
US-08-222-177A-400
: Sequence 400, Application US/08222177A
: Patent No. 5582979
: Patent INFORMATION:
PAPLICANT: Weber, James L.
PAPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
UMBER OF SEQUENCES: 460
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-222-177A-119
; Sequence 119, Application US/08222177A
; Patent No. 5582979
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MEDIDM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,177A
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/341,562
FRIOR APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1999
ATTORNEY/ACENT INFORMATION:
NAME: Sata, Charles S.
REGISTRATION NUMBER: 09865.601
TELEPRONE: (608) 831-2100
TELEPAX: (608) 831-2106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:

APPLICANT: Weber, James L.

TITLE OF INVENTION: (LENGTH POLYMORPHISMS IN

TITLE OF INVENTION: (GC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME

NUMBER OF SEQUENCES: 460

CORRESPONDENCE ADDRESS:

ADDRESSEE: DeWitt Ross & Stevens, S.C.

STREET: 8000 Excelsior Drive, Suite 401

CITY: Madison

STATE: Wisconsin

COUNTRY: USA

TIP: 53717-1914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 119:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMMEDIATE SOURCE:
CLONE: mfd23rs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
COMPUTER READABLE FORM:
                       COUNTRY: USA
ZIP: 53717-1914
                                                              CITY: Madison
STATE: Wisconsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.1%; Score 36; DB 1; L
Local Similarity 100.0%; Pred. No. 0.00084;
les 36; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                               2 CACACACACACACACACACACACACACACACACA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
E: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 40;
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RESULT 9
US-08-222-177A-403
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Matches
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SEQUENCE CHARACTERISTICS:
LENGTH: 40 base pairs
TYPE: nucleic acid
TYPE nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION PATENTION
APPLICATION NUMBER: US/08/222,177A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US/08/222,177A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 07/341,562
APPLICATION NUMBER: US 07/341,562
APPLICATION NUMBER: 30,492
REGISTRATION NUMBER: 30,492
REGISTRATION NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
TELEFAX: (608) 831-2106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 403, Appl
Patent No. 5582979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Ouery Match
Best Local Similarity 100.0%; Pred. No. 0.00084;
Matches 36; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: SATA, Charles S.
REFERENCE/DOCKET NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,177A
FILING DATE: ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: DeWitt R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Weber, James L.
TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NERAL INFORMATION:
APPLICANT: Weber,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 8000 Exce
CITY: Madison
STATE: Wisconsin
                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 53717-1914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (608) 831-2106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 CACACACACACACACACACACACACACACACA 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: DeWitt Ross & Stevens, S.C. 8000 Excelsior Drive, Suite 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/08222177A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA (genomic)
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SEQUENCE CHARACTERISTICS:

403:

LENGTH:

40 base pairs

nucleic acid

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Patent No. 5582979
GENERAL INFORMATION:
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Best Local
                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341
FILING DATE: 21 APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 0986
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 41 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                 CLONE: mfd8rs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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 CACACACACACACACACACACACACACACACACA 36
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                                                                                                                                                                                        nucleic acid
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8000 Excelsior Drive, Suite 401
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                              Conservative
                                                                                                                                                             linear
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                                                                                                                                                                            double
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100.0%; Pred. No.
tive 0; Mismatc
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                                         0.1%; Score 36;
100.0%; Pred. No.
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                                           DB 1; Le 0.00083;
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                                                        Length 41;
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; IMMEDIATE SOURCE:
; CLONE: mfd45rs
US-08-222-177A-183
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                                                                                                                                  Sequence 232, Application US/08222177A Patent No. 5582979
                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                       Query Match
                                             GENERAL INFORMATION:
APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUEN
NUMBER OF SEQUENCES: 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0.
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (608) 831-2100
                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 53717-1914
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Sara, Charles S. REGISTRATION NUMBER: 30,492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                      1 CACACACACACACACACACACACACACACACACA 36
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es 36; Conservative
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82979
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E: DeWitt Ross & Stevens, S. 8000 Excelsior Drive, Suite
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           double
                                                                                                                                                                                                                                                                                                                     0.1%; Score 36;
100.0%; Pred. No.
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LENGTH POLYMORPHISMS IN
(dC_dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
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                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                  SEQUENCES
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                                                                  AND METHODS OF USING SAME
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CITY: Madison STATE: Wisconsin

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US-08-222-177A-53
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                                                                                                                                                                                                                                                                                                                                          Sequence 53; Application US/08222177A

Patent No. 5582379

GENERAL INFORMATION:
APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dc-dA)n.(dd-dT)n SEQUENCES AND METHODS OF USING SAME
RUMBER OF SEQUENCES: 460
CORRESPONDENCE ADDRESSE: DeWitt Ross & Stevens, S.C.
ADDRESSEE: BOOD Excelsior Drive, Suite 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/222,177A
FILING DATE:
CLASSIFICATION UNMBER: US/08/222,177A
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sata, Charles S.
REGISTRATION UNMBER: 30,492
REGISTRATION UNMBER: 30,492
REGISTRATION UNMBER: 09865.601
TELEPHONE: (608) 831-2100
TELEPAX: (608) 831-2106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 0.1%; Score 36; DB 1; L
Best Local Similarity 100.0%; Pred. No. 0.00083;
Matches 36; Conservative 0; Mismatches 0;
APPLIANCE
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: DNA IMMEDIATE SOURCE: CLONE: mfd63rs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                     COUNTRY: USA
ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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LENGTH: 41 base pairs
                                                                                                                                                                                                                                                                                                  CITY: Madison
STATE: Wisconsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA (genomic)
                                      US 07/341,562
                                                                                                                    US/08/222,177A
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RESULT 14
US-08-222-177A-229
; Sequence 229, Application US/08222177A
; Patent No. 5582979
; PATENT INFORMATION:
; APPLICANT: Weber, James L.
; APPLICANT: TRANSPON: LEMGTH POLYMOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: DI
; IMMEDIATE SOURCE:
; CLONE: mfdlrs
US-08-222-177A-53
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INFORMATION FOR SEQ ID NO: 5

SEQUENCE CHARACTERISTICS:

LENGTH: 42 base pairs

TYPE: nucleic acid

TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                      COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, v
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,177A
FILING DATE:
FILING DATE: US/08/2341,562
FRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/341,562
FRIUNG DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REFERENCE/DOCKET NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Sara, Chailes S.
REGISTRATION UNMER: 30,492
REFERENCE/DOCKET NUMBER: 0986
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
TELEFAX: (608) 831-2106
                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: C
TOPOLOGY: lines
MOLECULE TYPE: DN
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: LENGTH POLYMORPHISMS IN TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME NUMBER OF SEQUENCES: 460
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 8000 Excel
CITY: Madison
STATE: Wisconsin
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                        TELEFAX: (608) 831-2106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 53717-1914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                      linear
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                    DNA (genomic)
                                                           double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.1%; Score 36; DB 1; I
100.0%; Pred. No. 0.00083;
7ative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                        US 07/341,562
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Release #1.0, Version #1.25
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TELEX:
TELEX:
INFORMATION FOR SEQ ID NO: 388:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLOME: mfd123rs
US-08-222-177A-388
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US-08-222-177A-229
Search completed: March 29, 2000, 12:57:56 Job time: 32938 sec
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US-08-222-177A-388
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Patent No. 5582979

GENERAL INFORMATION:
APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 460
CORRESPONDENCE ADDRESS:
ANDRESCEPT. TOTALL TO THE TOTALL TO
                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.1%; Score 36; DB 1; Length 43; Best Local Similarity 100.0%; Pred. No. 0.00083; Matches 36; Conservative 0; Mismatches 0; Indels
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/341,562
APPLICATION NUMBER: US 07/341,562
APPLICATION NUMBER: US 07/341,562
APPLICATION INFORMATION:

NAME: Sara, Chailes S.

REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
TELEFAX: (608) 831-2106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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ZIP: 53717-1914
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STATE: Wisconsin
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                                                                                                                                                                                                            E: DeWitt Ross & Stevens, S.C.
8000 Excelsior Drive, Suite 401
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammal:
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 103)

Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, J.
Parsons, J., Rifkin, L., Rohifing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. an,
Milson, R.
                                                                                                                                                                                                                                                                            T77382 103 bp
yd72h12.r1 Soares fetal
IMAGE:113831 5' similar
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A0335255 co66611.2
A0335255 co66611.2
A0335255 co66611.2
A0335255 co66611.2
A0450144 Homo sspi
F24490 HSPD10834 H
B65983 CIT.-195-669
B05985 CST.-195-56
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B65983 CIT.-19605.7
A04078242 7H16605.7
A04078241 A468 me30h05.7
A0407824 A468 me30h05.7
A0407824 A468 me30h05.7
A0407824 A468 me30h05.7
A0582186 RPCI-11-3M4.
A0478256 RPCI-11-3M4.
A0478262 CSRL-1506.3
A0479532 VS94-603.7
A0407826 CYSL-1506.3
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103 TGAGAGTCTCACTCCACTGCAACCTCCCCCTCCTATATTCAAGTGATTCTCTTGCCTCA 44
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 95)

S Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Hulman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.

The Washb-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: estevatson.wustl.edu
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l Similarity 100.0%;
80; Conservative (
                                                                                                                                                                                                                                                                                                       R08388 95 bp mRNA EST 05-APR-1995 yf19d03.rl Soares fetal liver spleen INFLS Homo sapiens CDNA clone IMAGE:127301 5' similar to gb:M60750_cds1 HISTONE H2B (HUMAN);,
                                                                                                                                                                                                                      Homo sapiens
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                                          Unpublished (1996)
On Sep 12, 1996 this sequence version replaced Contact: Marra M/Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, 17e1: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cione is available royalty-free through LLNL; contact the Consortium (info@image.llnl.gov) for further information. Insert Length: 727 Std Error: 0.00 Seq primer: M13RP1
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v190a02.rl Stratagene mouse hea
IMAGE:919466 5', mRNA sequence.
AA500598
                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 89)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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Location/Qualifiers
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Insert Size: 727
                                                                                                                                                                                                                                                                                                                    house mouse.
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clone is available royalty-free through LLNL; contact the
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                mouseest@watson.wustl.edu
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/clone="IMAGE:127301"
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7 100.0%; Pr
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Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. J
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
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1 (bases 1 to 95)
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IMAGE:67887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMAGE Consortium (info@image.llnl.gov) for further information. MGI:531682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Other_ESTs: ya79d08.s1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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//tissue_type="heart"
//dev_stage="13 day embryos"
//lab_host="SOIR (Kanamycin resistant)"
//lab_host="SOIR (Kanamycin resistant)"
//note="forgan: heart; Vector: pBluescript SK-; Site_1:
//note="forgan: heart; Vector: pBluescript SK-; Site_1:
//note="forgan: heart; Vector: pBluescript SK-; Site_1:
//note="forgan: heart; Vector: pBluescript Site_1: heart; Cloned unidirectionally. Primer:
//oligo dT. 93 pooled NHJ/Swiss 13 day embryo hearts.
//oligo dT. 93 pooled NHJ/Swiss 13 day embryo hearts.
//note="forgan: heart; Vector: pBluescript SK-; Site_1:
//note="forgan: heart; Vector: pBluescript SK-; Site_1: heart; Vector: pBluescript SK-; Site_1:
//note="forgan: heart; Vector: pBluescript SK-; Site_1: heart; Vector: pB
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/strain="NIH/Swiss"
/db_xref="taxon:10090"
/clone="IMAGE:919466"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Stratagene mouse
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7 5' similar to contains Alu
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Pred. No.
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0.018;
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AQ006534/c
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                                                                                                                                                                                                                                                                                                                9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1997)
Other GSSs: CIT-HSP-2054B16.TR.1 CIT-HSP-2054B16.TR
CONTACT: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota: Metazoa: Chordata: Craniata; Vertebrata; Mammalia; Eutheria: Primates: Catarrhini; Hominidae; Homo.

1 (bases 1 to 101)

1 Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Gaden, K., Berry, K., Granger, D., Suh, E., Wible, C., Kim, U.-J., Shizuya, H., Simon, M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        genomic survey sequence
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CIT-HSP-2054B16.TF CIT-HSP
                                                                                                                                                                                                                     http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13-21;
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQ006534.1 GI:3081351
                                                                                                                                                                                                                                                                                      Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
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                 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="CIT-HSP"
/sex="Male"
/sex="Male"
/cell_type="Sperm"
/note="Yector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                  /db_xref-"taxon:9606"
/clone-"2054B16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
/clone="IMAGE:67887"
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/db_xref="GDB:504144"
                                                                                                                                                 /organism="Homo sapiens"
/db_xref="GDB:7057963"
                                                                                                                                                                                                     Location/Qualifiers
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Pred. No. 0.037;
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Homo sapiens genomic clone 2054B16
                 40 t
                                                                                                                                                                                                                                                                                                                                                        MD 20850, USA
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 QY 24632 CCATTGCACTCCAGCCTGGGCAACAAGAGCAAAACTC 24668
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Query Match Best Local S Matches 37

Local Similarity nes 37; Conserv

Conservative

0.1%; Score 37; 100.0%; Pred. No.

DB 40; Length 54; 0.11; 0

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0; Mismatches

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AA935225/c
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Ouery Match
Best Local Similarity 100.0%; Pred. No. 0.036;
Matches 38; Conservative 0; Mismatches 0; Indels
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On Jan 14, 1998 this sequence version replaced gi:1797423.
On Jan 14, 1998 this sequence version replaced gi:1797423.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
Emmert-Brocurement: Christopher A. Moskaluk, M.D., Ph.D., Mic
Emmert-Buck, M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CONNA Library Arrayed by: Greg Lennon, Ph.D.
CON
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 54)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Insert Length: 490 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
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                                 /note-"vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; lst strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1571133"
/clone_lib="NCI_CGAP_GC4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="pooled germ cell tumors"
/lab_host="DH10B"_____
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                                                ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Primates; Catarrhini; Hominidae; Homo.
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DKFZp434P234)
                                                                                                                                                                                                                                                                                                                                                                                                                                             sl sequence also available
This clone is available at the RZPD in Berlin
Please contact the RZPD: Ressourcenzentrum, Heubnerweg
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-MAR-1999
12-MAR-1999
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  Eukaryota; Metazoa; (Eutheria; Primates; (bases 1 to 80)
Lanfranchi, G., Murar
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/clone="DKF2p434P234"
/clone_11b="434 (synonym: h
DH10B; sites Noti + Sali"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence
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                                                                                   GI:4810116
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  Muraro, T.,
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Catarrhini; Hominida
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   Pacchioni, B.,
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   Pallavicini, A.,
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AA598741/c
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                                                                                                                                                                                                                                                                        AA598741 89 bp mRN
ae49g12.s1 Stratagene lung
IMAGE:950278 3' similar to
                                                                                                         Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jos. Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. WashU-NCI human EST Project
                                                                                                                                                                                                                                                                                                                                                                                                            37; Conserv
                        Tel: 314 286 1800
Fax: 314 286 1810
                                               Washington University School of Medicine
                                                                                              Unpublished (1997)
                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 89)
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Location/Qualifiers
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                                                                         Contact: Wilson RK
                                                                                    On May 18,
                                                                                                                                                                                                        Homo sapiens
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    clone
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Conservative
est@watson.wustl.edu
lone is available royalty-free
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="s4000013A06"
/clone_lib="HM3"
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                                                                                   1995 this sequence version replaced
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gi:811447

Jost, S.,

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Pandolfo,D., Toppo,S., Trevisan,S., Scarso,S. and Valle,G. Identification of 4370 expressed sequence tags from a 3'-end-specific cDNA library of human skeletal muscle by DNA sequencing and filter hybridization genome Res. 6 (1), 35-42 (1996) 96276048
On Jun 5, 1998 this sequence version replaced gi:3188834.
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ABI Chromatograms and other information are available on WWW
                                                                                                                                                                                                                                                                                                                                                                                 non-palindromic BstXI adapters, NotI digested and directionally cloned into BstXI-NotI cut pcDNAII _{1} 21 c 19 g 22 t
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Best Local Similarity 100.0%;
Matches 37; Conservative
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Seq pi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
Contact: Ung-Jin Kim
Callech Genome Research Lab
California Institute of Technology
Division of Biology, MS 147-75, Pasadena, CA 91125, USA
Tel: 626 796 7066
Fax: 626 395 4901
Email: ung@ash.tree.caltech.edu
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1 (bases 1 to 102)
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http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
seq primer: SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: ung@ash.tree.caltech.edu
Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kim, U.-J., Adams, M.D. and Simon, M.I.
Determination of clone end sequences of human Bacterial Artificial
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/db xref="taxon:9606"
/db xref="taxon:9606"
/clone=11b="Stratagene lung carcinoma 937218"
/clone=11b="Stratagene lung carcinoma"
/cell_line="NGLE:169"
/dev_stage="cell line NCI-H69"
/lab_host="SOLR (kanamycin resistant)"
/lab_h
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                                                                            /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                     /db_xref="taxon:9606"
/clone="669F15"
                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="GDB:5491647"
                                                                                                                                                                                                                                                                                                                                                    Cocat
                                                                                                                                                                          /clone_lib="CIT-HSP"
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                       21 g
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AUTHORS
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AI262095
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Matches 37; Conserv
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                                                                                                                                                                                                                                                                 11 CACACACACACACACACACACACACACACACACACA 46
                                                                                                                                                                                                                                                                                                                      1 CACACACACACACACACACACACACACACACACACA 36
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1 (bases 1 to 58)

1 (bases 1 to 58)

Evans.G.A., Burbee, D., Davies, C., Habner, L., Oliver, T., Gilbert, M., Jones, D., Ward, T., Gillilan, E., Schagemann, J., Probst, S., Harris, J., DeFord, J., McFarland, J., Burzinski, K., Khan, M., Kupfer, K. and Garner, H.R. Genomic Sequence Sampled Map of Chromosome 11

Onpublished (1996)

Onpublished (1996)
                                                  AI262095 80 bp mRNA EST 13-NOV-1998 qz28c05.yl NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2028200 5' similar to contains Alu repetitive element;contains TAR1 repetitive
                                                                                                                                                                                                                                                                                                                                                                               1 Similarity
36; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B03985 13-JUL-1996 CSRL-21b5-u CSRL flow sorted Chromosome 11 specific cosmid Homo spiens genomic clone cSRL-21b5, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Evans GA, Shane Probst
McDermott Center for Human Growth and Development
University of Texas Southwestern Medical Center At
5323 Harry Hines Blvd, Dallas TX 75235-8591
Tel: 214-648-1600
Fax: 214-648-1666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: gevanseutsw.swmed.edu, shaneemcdermott.swmed.edu
Seg primer: T7
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                          ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cell_type="chimeric hamster somatic cell hybrid"
/note="Vector: SCos-1; Human Chromosome 11 specific cosmid
library prepared from flow sorted human Chromosome 11
derived from Chinese Hampster Ovary (CHO) monochromosomal
somatic cell hybrid, J1" 5 t 1 others
a 24 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="cSRL flow sorted Chromosome 11 specific cosmid"
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/db_xref="taxon:9606"
/clone="cSRL-21b5"
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                                                                                                                                                                                                                                                                                                                                                                                                      0.1%; Score 36; DB 81; 100.0%; Pred. No. 0.23;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCCAGGCTGGAGTGCAGTGGCACGATCTTGGCTCAC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36;
1 (bases 1 to 84)
Lanfranchi,G., Muraro,T., Caldara,F., Pacchioni,B., Pallavic Pandolfo,D., Toppo,S., Trevisan,S., Scarso,S. and Valle,G. Identification of 4370 expressed sequence tags from a 3'-end'specific cDNA library of human skeletal muscle by DNA sequencing and filter hybridization
                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HSPD29754 HM3
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 80)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGA
                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13
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/clone="IMAGE:2028200"
/clone_lib="NCI_CGAP_Kidll"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:4820260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA clone sH3-000CO2-1/FO6, mRNA
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                                                                                                                                                               Pallavicini, A.,
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                                                                                                                                                                                                                                                                         Contact: Eric D. Green Genome Technology Branch National Human Genome Research Institute/NIH 49 Convent Dr., MSC4431, Building 49, Room 22 Tel: 3014020201
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96276048
On Jun 5, 1998 this sequence version replaced gi:3188981.
contact: Valle G.
                                                                                                                                                   Email: egreen@nhgri.nih.gov
Plate: 16 row: G column:
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7H16G05, mRNA sequence
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ABI Chromatograms and other information are available on WWW
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                                                                                     primer: -21M13 (ABI).
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/note="Vector: pcDNAII (Invitrogen); Site_1: BstXI;
Site_2: NotI; The library was constructed by G.
Lanfranchi. This library is not subtracted nor normalized.
The first strand cDNA was primed with a biotinylated
oligo-dT-NotI primer
(5'-biotin-AACCCGGCTCGAGCGGCCGCTTTTTTTTTTTTTTTT-3'). The
    /organism="Homo sapiens"
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/clone_lib="HM3"
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/db_xref="taxon:9606"
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Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 8)
1 (bases 1, Jost, Jost, Jost, Jost, Jost, Jost, S., Jan, F., Jost, Jose, Jose, Jose, Jost, Jose, Jose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
On May 18, 1995 this sequence version replaced gi:811447.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA598741 19-DEC-1997
AA598741 89 bp mRNA
ae49912.sl Stratagene lung carcinoma 937218 Homo saplens cDNA clone
IMAGE:950278 3' similar to contains Alu repetitive element; mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: 40ml3 fwd. ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
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/cell_line="HeLa cell line; ATCC"
//lab_host="E. coll strain DHS alpha"
//lab_host="E. coll strain DHS alpha"
//note="Vector: pAMP10; cDNA, was generated from cytoplasmic RNA using a mixture of random DNA hexamers and oligo(dT).
From this pool of cDNA, human chromosome 7-enriched cDNA was isolated by direct cDNA, selection using chromosome 7 genomic DNA (cosmids). The resulting direct selected cDNA was cloned into a plasmid vector using a non-directional uracil DNA glycosylase (UDG)-mediated cloning strategy."
a 0 c 45 g 44 t
                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
//db_xref="taxon:9606"
//clone="rthggE:950278"
//clone=11b="Stratagene lung carcinoma 937218"
//tissue_type="lung carcinoma"
//cell_line="NCI-H69"
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/clone_lib="Chromosome 7 HeLa cDNA Library" /sex="female"

/db_xref="taxon:9606" /clone="7H16G05"

Query Match
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Matches 36; Conserv 0.1%; Score 36; DB 36; Length 89; liarity 100.0%; Pred. No. 0.17; Conservative 0; Mismatches 0; Indels 0

Gaps

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QY 1219 CCCAGGCTGGAGTGCAATGGCGCGCATCTTGGCTCAC 12234
Db 28 CCCAGGCTGGAGTGCAATGGCGCGATCTTGGCTCAC 63

Search completed: March 29, Job time: 11411 sec 2000, 06:25:57

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12428.204 Million cell updates/sec
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; Mismatches 0;

Indels

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Gaps

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DATE DATE

Q33849 standard; DNA; 70 BP.
Q33849;
Q2-FEB-1993 (first entry)
Microsatellite sequence from clone TGLA26.
PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.

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Weber JL; WPI; 97-042299/04. WPI; 97-042299/04. PI Detection of polymorphic genetic markers of the form Detection of polymorphic nucleic acid mols. as primers (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers primers placed primers (dC-dA)n. (dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commaning the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) probe. Over 100 repeat blocks were isolated by hybridisation for purbe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by pinners T65798-T66047. Those clones where the repeat sequence has been determined are shown in T65704-797. This repeat sequence is from the marker clone Mdf33 which contains the repeat Sequence 56 BP; 28 A; 27 C; 0 G; 1 T;	<pre>marker clone Mfd33. enetic marker; primer; paternity; maternity; ! e; animal; plant; bree</pre>	NNENTS	
repeat sequence d as genetic d as genetic ty testing lity testing list clones disastion of boly(dC-dA). (dG boly(dC-dA). (dG boly(dC-dA)). (dG	amplification human; pedigre ding; locus;	Synthetic oligonuc Synthetic oligonuc Analytical solid p Self-complementary Sequence binding t Neural thread prot	Human mitochondria Primer for mitocho Primer for mitochondria Human mitochondria Homo sapiens clone Belor complementary

Best Local Similarity 100.0%; Matches 40; Conservative 0;

Pred. No. 0.
; Mismatches

0.00042; hes 0;

Indels

0;

Gaps

0

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RESULT
V19044/c
ID V190
AC V190
DE Alu
DE Alu
KW Circ
OS Synt
Sector
OS Synt
KW Circ
OS Sector
O
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PD 99-JUL-1996; W0-11478.

PP 09-JUL-1996; W0-011478.

PR 09-JUL-1996; W0-011478.

PR (USSH) US DEPT HEALTH & HUMAN SERVICES.

PA (USSH) 
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PA (GE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.2%;
Best Local Similarity 100.0%;
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alu PCR primer 1.
PCR; primer; amplification; Alu repeat sequence; vector; circular yeast artificial chromosome; YAC; ss. Synthetic.
Saccharomyces sp.
W09801573-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-AUG-1992.
15-JAN-1992; U00340.
15-JAN-1991; US-642342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              V19044 standard; DNA; 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
o. 0.00018;
O; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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Matches 3
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Best Local :
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Query Match

Score 40;

DB 1;

Length 40

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PA (WARS) JARSHIPELD CLINIC.

PA (WARS) JARSHIPELD CLINIC.

DR WPI; 97-042299/04.

DR WPI; 97-042299/04.

PI (dC-dA)n(dG-dT)n - using novel nucleic acid mois. as primers of cd-dA)n(dG-dT)n - using novel nucleic acid mois. as primers primers listic primers to the isolation of polymorphic repeat sequences of the invention relates to the isolation of polymorphic repeat sequences comparing the sequence (GC-dA)n, (GG-dT)n which can be used to detect these crepeats, especially for use in e.g paternity or maternity testing, commarkers. Primers based on these sequences can be used to detect these crepeats, especially for use in e.g paternity or maternity testing, commarkers. Primers based on these sequences analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of cromosome-specific phage libraries with a synthetic poly(CC-dA).(dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers T65798-T66047. Those clones where the repeat sequence has been determined are shown in T65704-797. This repeat compared to the marker clone wdf12 which contains the repeat compared to the communia. (AC)11AT(AC)8A.

Sequence 39 BP; 20 A; 18 C; 0 G; 1 T;
                   06-AUG-1992; U00340.
15-JAN-1992; U00340.
15-JAN-1991; US-642342.
(GENM-) GENMARK.
GEOTGES M. MASSEY JM;
RPI; 92-84684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
US582979-A.
10-DEC-1996.
21-APR-1989; 341562.
21-APR-1989; US-341562.
05-SEP-1991; US-754351.
04-APR-1994; US-222177.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Microsatellité sequence from clone TGLA400. PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss. Bos taurus. WO9213102-A.
                                                                                                                                                                                                                                                                                                                                     034003 standard; DNA; 50 BP. 034003; 02-FEB-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat sequence from polymorphic marker clone Mfd12.

Polymorphism; repeat sequence; genetic marker; priner; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4/c
T65714 standard; DNA; 39
Polymorphic bovine DNA markers - used in genetic identification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 0.2%; So smilarity 100.0%; I similarity 100.0%; I 39; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 39; DB 1; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
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PRESENTE OF THE PRESENT OF THE PRESE
                                                                                                                                                                                                                                               programming, and selective breeding

Programming, and selective breeding

Table 7; Page 371; 517pp; English.

CC The sequence is that of a bovine microsatellite sequence obtd.

CC by screening a library of bovine MooI DNA fragments of between

CC 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.

CC One out of 50 clones cross-hybridised. Assuming independent

CC (15)n >9 microsatellites in the bovine genome is estimated at >100,

CC (16)n >9 microsatellites in the bovine genome is estimated at >100,

CC (16)n >9 microsatellites in the bovine microsatellites

CC (16)n >9 microsatellites in the bovine microsatellites

CC (16)n >9 microsatellites in the bovine microsatellites

CC (16)n >9 microsatellites in the specification and indexed herein (see below).

CC (17)n >9 microsatellites may be used to introcatellite sequence

CC were used to generate the required PCR primers for in vitro

CC amplification of the corresp. microsatellite (using the program

CC (16)n parentage testing, and in the genetic mapping of economic trait

CC (16)n parentage testing, and in the genetic mapping of economic trait

CC (16)n parentage testing, and in the genetic mapping of economic trait

CC (16)n parentage testing, and in the genetic mapping of economic trait

CC (16)n parentage testing, and in the genetic mapping of economic trait

CC (16)n parentage testing, and in the genetic mapping of economic trait

CC (16)n parentage testing, and in the genetic mapping of economic trait

CC (16)n parentage testing, and in the genetic mapping of economic trait

CC (16)n parentage testing, and in the genetic mapping of economic trait

CC (16)n parentage testing, and in the genetic mapping of economic trait

CC (16)n parentage testing, and in the genetic mapping of economic trait

CC (16)n parentage testing the program of the program of the parentage testing the program of the parentage testing the program of the parentage testing the program of the prog
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PT Table 7; Page 331; 517pp; English.
CC The sequence is that of a bovine microsatellite sequence obtd. by
CC Screening a library of bovine MboI DNA fragments of between
CC 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.
CC One out of 50 clones cross-hybridised. Assuming independent
CC distribution of microsatellites and MboI sites, the frequency of
CC (T6)n >9 microsatellites in the bovine genome is estimated at >100,
CC 000. The sequence information for ca. 230 such bovine microsatellites
CC is summarised in the specification and indexed herein (see below).
CC The sequences upstream and downstream of the microsatellite sequence
CC were used to generate the required PCR primers for in vitro
CC amplification of the corresp. microsatellite (using the program
CC OPTIFRIM). The microsatellites may be used to identify individuals,
CC for parentage testing, and in the genetic mapping of economic trait
CC traits esp. in cattle, to allow selective breeding.
CC See also Q33501-34437.
CC Sequence 50 BP; 1 A; 2 C; 22 G; 25 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 38
    Query Match 0.3
Best Local Similarity 100
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENM-) GENMARK.
Georges M, Massey JM;
WPI; 92-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI: 92-284684/34.
Polymorphic bovine DNA markers - used in genetic identification.
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02-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence of a microsatellite from clone TGLA58. PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q34100 standard; DNA; 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L5-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L5-JAN-1992; U00340
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                                                                                                                                                                                                                             BP;
                                        0.2%;
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Score 38; DB Pred. No. 0.0
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                                                                                                                                                                                                                    0 C;
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Pred. No.
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                                                                                                                                                                                                                    27
                                             DB 1;
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0.0017;
                                                                                                                                                                                                                    <u>ن</u>
                                             .0017;
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RESULT
Q27391
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Q27391
AC
Q27391
Q2
AC
Q27

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T65736/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DR WPI; 97-042299/04.

PDE tection of polymorphic genetic markers of the form procedure of polymorphic genetic acid mols. as primers (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers from the invention relates to the isolation of polymorphic repeat sequences. The invention relates to the isolation of polymorphic repeat sequences (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g. paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA).(dG-dT) grobe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers T65798-T66047. Those clones where the repeat sequence has been determined are shown in T65704-797. This repeat sequence is from the marker clone Mdf34 which contains the repeat sequence having the formula: (AC)4AT(AC)15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-DEC-1996.
21-APR-1989; 341562.
21-APR-1989; US-341562.
05-SEP-1991; US-754351.
04-APR-1994; US-222177.
                                                                                                                                                                                                                                                                                                                        Synthetic.
W09213101-A.
06-AUG-1992.
                                                                  Ultterlinden AG, Vijg J;
WPI; 92-284633/34.
Detection of genetic variation by 2-D electrophoresis of fragments - and hybridisation with labelled probes, carried fragments - onesisting of inter-repeat sequences generated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T65736 standard; DNA; 40 T65736;
   Claim 6; Page 6; 31pp; English
Primer PDJ33 is one of several
                                                                                                                                                                                                                                   24-JAN-1992; NL0018.
25-JAN-1991; NL-000132.
(INGE-) INGENY BV.
                                                                                                                                                                                                                                                                                                                                                                                                                Polymerase chain reaction; PCR; repetitive element;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Repeat sequence from polymorphic marker clone Mfd34.

Rolymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Inter-Alu specific primer PDJ33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-JAN-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Weber JL;
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US5582979-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MARS-)
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les 36; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MARSHFIELD CLINIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.2%;
llarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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Pred. No.
   primers which
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0.008;
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      are
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   preferred
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      for use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PA (GENM) JGENNARK.

PA (GENM) JGENNARK.

DR WPI; 92-284684/34.

DR WPI; 92-284684/34.

PT Polymorphic bovine DNA markers - used in genetic identification, price mapping, and selective breeding gene mapping, and selective breeding rable 7; Page 213; 517pp; English.

CThe sequence 1s that of a bovine microsatellite sequence obtd. by cc screening a library of bovine Mbol DNA fragments of between common to the sequence in the sequence Mbol DNA fragments of between common to follow by the analysish.

CC one out of 50 clones cross-hybridised. Assuming independent clistribution of microsatellites and Mbol sites, the frequency of common to follow by the sequence information for ca. 230 such bovine microsatellites common is estimated at >100, common to the sequence information and indexed berein (see below).

CC one sequences upstream and downstream of the microsatellite sequence complification of the corresp. microsatellite (using the program complification of the corresp. microsatellite (using the program complification of the corresp. microsatellite (using the program complification that the sequence in the genetic mapping of economic trait compliments for in vitro and in the genetic mapping of economic trait compliments of the control trait compliments of the control trait to compliment compliments for in vitrol compliments.

CC of pripring the program of the program o
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Best Local S
Matches 35
                                                                                                                                                                                                                                                                                                                                                        Query Match 0.2%;
Best Local Similarity 100.0%;
Matches 35; Conservative
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                                                               7/c
765737; standard; DNA; 45 BP
765737;
17-JUN-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-AUG-1992.
15-JAN-1992; U00340.
15-JAN-1991; US-642342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-FEB-1993 (first entry)
Microsatellite sequence from clone TGLA134.
PCR; selection; priners; OPTIPRIM; breeding; cattle; parentage;
genetic mapping; traits; amplification; ss.
Repeat sequence from polymorphic marker clone Mfd36. Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree
                                                                                                                                                                                                                                                      Q33713 standard; DNA; Q33713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 Similarity 100.
35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.2%;
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                                                                                                                                                                                                                                                                                                                                                        Score 35; DB Pred. No. 0.0 0; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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0.017;
                                                                                                                                                                                                                                                                                                                                                                                 0.017;
                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 35
                                                                                                                                                                                                                                                                                                                                                          0
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        human; pedigree;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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RESULT 11
033870
AC 033870
AC 033870
DT 02-FEB
DE Micros
KW PCR; s
KW PCR; s
SKW PCR; s
PCR 15-JAN
PA (GENN-
PI GEOING
PF 15-JAN
PA (GENN-
PI GEOING
PF POLYMC
PT POLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PT Detection of polymorphic genetic markers of the form PT (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers PT (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers PS Disclosure; Column 9-10; 186pp; English.

PS Disclosure; Column 9-10; 186pp; English.

CC having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic CC markers. Primers based on these sequences can be used to detect these CC repeats, especially for use in e.g paternity or maternity testing, CC human genetic annlysts such as linkage analysis of genetic disease, CC commercial animal or plant breeding or pedigree analysis. Clones CC containing the repeat sequences were isolated by hybridisation of CC chromosome-specific phage libraries with a synthetic poly(GC-dA).(dG-dT) CC probe. Over 100 repeat blocks were isolated. The inserts from the clones CC were amplified by primers T6598-T66047. Those clones where the repeat sequence has been determined are shown in T65704-797. This repeat CC sequence is from the marker clone Mdf36 which contains the repeat CC sequence having the formula: (AC)15A7 (AC)16A.

SQ Sequence 45 BP; 23 A; 21 C; 0 G; 1 T;
prigne mapping, and selective breeding
Prable 7; Page 277; 517pp; English.

CC The sequence is that of a bovine microsatellite sequence obtd. by
CC screening a library of bovine mbol DNA fragments of between
CC 50 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.
CC 0ne out of 50 clones cross-hybridised. Assuming independent
CC (T6)n >9 microsatellites in the bovine genome is estimated at >100,
CC (00). The sequence information for ca. 230 such bovine microsatellites
CC is summarised in the specification and indexed herein (see below).
CC the sequences upstream and downstream of the microsatellite sequence
CC were used to generate the required PCR primers for in vitro
C amplification of the corresp. microsatellite (using the program
CC optiprim). The microsatellites may be used to identify individuals,
CC loci, or genes involved the determinism of economically important
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-APR-1989; 341562.
21-APR-1989; US-341562.
05-SEP-1991; US-754351.
04-APR-1994; US-222177.
(WARS-) MARSHFIELD CLINIC
Weber JL;
WPI; 97-042299/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OZ-FEB-1993 (first entry)
OZ-FEB-1993 (first entry)
Microsatellite sequence from clone TGLA272.
Microsatellite sequence from clone TGLA272.
PCR; selection; primers; oPTIFRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
Bos taurus.
W05013102-A.
06-AUG-1992: U00340.
15-JAN-1991: U00340.
15-JAN-1991: U5-642342.
(CENM-) GENMARK.
(GENTS) GENMARK.
Georges M. Massey JM;
WPI; 92-284684/34.
Polymorphic bovine DNA markers - used in genetic identification,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7526 TGTGTGTGTGTATGTGTGTGTGTGTGTGTGTGTGT 7560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q33870 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MARSHFIELD CLINIC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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RESULT
1034050
10 AC 033
AC 033
AC 033
AC 033
AC 037
AC 03
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V19044
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PR 09-JUL-1996; W0-U11478.

PR (USSH) US DEPT HEALTH & HUMAN SERVICES.

PR (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI KOUPTINA NY, Larionov VL, Perkins EL, Resnick MA;

PI ROUPTINA NY, Larionov VL, Perkins EL, Resnick MA;

PT PROPAGATION USING Vector comprising yeast centromere, marker, pr recombination using vector comprising yeast tentromere, marker, pr yeast telomere and nucleic acid for recombination

PT Yeast telomere and nucleic acid for recombination

CC This is the nucleotide sequence for the PCR primer used in the Example 1; Page 45; 117pp; English.

CC This is the nucleotide sequence, which is used to amplification of the Alu repeat sequence, which is used to comprise the processes described in the invention. It involves the creation and use of circular yeast artificial chromosome (YAC) to selectively clone specific nucleic acids from a background of the selectively clone specific nucleic acids from a background of the creation be used to rapidly isolate human DNA where only a part of the sequence of DNA is known. Using the methods large fragments of DNA can be easily cloned and analysed.

So Sequence 40 BP; 7 A; 12 C; 13 G; 8 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 34
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Best Local Similarity
Matches 35; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10059 GCTCACGCCTGTAATCCCAGCACTTTGGGAGGCC 10092
                                                                                                       06-AUG-1992.
15-JAN-1992;
15-JAN-1991;
                           (GENM-) GENMARK.
Georges M, Massey JM;
WPI; 92-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7526
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See also Q33501-34437.
Sequence 54 BP; 1
                                                                                                                                                                                                                                 Microsatellite sequence from clone TGLA437. PCR; selection; primers; OPTIPRIM; breeding; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saccharomyces sp. WO9801573-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCR; primer; amplification; Alu repeat sequence; vector; circular yeast artificial chromosome; YAC; ss.
                                                                                                                                                                                      WO9213102-A.
                                                                                                                                                                                                                                                                                                                   02-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                       Q34050 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               V19044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     V19044 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTCACGCCTGTAATCCCAGCACTTTGGGAGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.2%;
Similarity 100.0%;
34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.2%;
llarity 100.0%;
Conservative
        bovine DNA markers
                                                                                                          U00340.
US-642342.
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                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                       DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA; 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 A;
                                                                                                                                                                                                                                                                                                                                                                       86 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 34;
Pred. No.
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V37197 standard; DNA; 80 V37197;

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PT gene mapping, and selective breeding
Table 7; Page 351; 517pp; English.

CT The sequence is that of a bovine microsatellite sequence obtd. by

CC Screening a library of bovine MboI DNA fragments of between

CC One out of 500 bp with an (AC)15 and a (TC)15 oligonuclectide probe.

CC One out of 50 clones cross-hybridised. Assuming independent

CC One out of 50 clones cross-hybridised. Assuming independent

CC (T6)n >9 microsatellites in the bovine genome is estimated at >100,

CC (T6)n >9 microsatellites in the bovine genome is estimated at >100,

CC out of sequence information for ca. 230 such bovine microsatellites

CC summarised in the specification and indexed herein (see below).

CC were used to generate the required PCR primers for in vitro

amplification of the corresp. microsatellite (using the program

CC optiprim). The microsatellites may be used to identify individuals,

CC for parentage testing, and in the genetic mapping of economic trait

CC loci, or genes involved the determinism of economically important

CC see also Q33501-34437.

SQ Sequence 86 BP; 11 A; 0 C; 40 G; 35 T;
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Best Local S
Matches 33
W69213101-A.
06-AUG-1992; NL0018.
24-JAN-1992; NL-00018.
25-JAN-1991; NL-000132.
(INGE-) INGENY BV.
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Q27391 standard; J
Q27391;
Q27391;
Q27-JAN-1993 (fir
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Inter-Alu specific p
Polymerase chain rea
Syntheti-
                                                                                                                                                                                                                                                                                                                                                               Claim 6; Page 6; 31pp; English.

Primer PDJ33 is one of several primers which are preferred for use in amplifying inter-Alu regions of DNA. The amplified fragments are then subjected to 2-D electrophoresis on the basis of length and differences in base sequence. The resulting separation pattern is transferred to a filter for screening with a probe. The method can
                                                                                                                                                                                                                                                                             be used to detect genetic variation.
See Q27389-Q27404 and Q33141-Q33144.
Sequence 35 BP; 8 A; 10 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detection of genetic variation by 2-D electrophoresis fragments - and hybridisation with labelled probes, con fragments consisting of inter-repeat sequences general
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ic primer PDJ33.
reaction; PCR; repetitive element;
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Name (1981) 635 Al.

PN (1981) 635 Al.

PD 23-APR-1998.

PF 17-CCT-1996; JP-274855.

PR 17-CCT-1996; JP-27485.

PR 17-CCT-1996; JP-27486.

PR 17-CCT-1996; JP-27486.

PR 17-CCT-1996; JP-27486.

PR 17-C
                                                                   Query Match 0.2%; Score 33; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 33; Conservative 0; Mismatches
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Oligonucleotide sequence of the specification.
Genotype; phenotype; molecular evolutionary engineering;
functional biopolymer; virus; ss.
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No. 0.064; 0; Indels
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Search completed: March 29, 2000, 17:55:02 Job time: 50700 sec

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1: /cgn2_6/ptodata/

2: /cgn2_6/ptodata/

3: /cgn2_6/ptodata/

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10455.780 Million cell updates/sec
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   GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-454-557C-57
US-08-454-5673C-57
US-08-454-5673C-57
US-08-454-5673C-57
US-08-454-557C-69
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US-08-455-673C-92
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US-08-456-673C-92
US-08-456-673C-92
US-08-113-646-444
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             Sequence 149, App
Sequence 27, Appl
Sequence 1, Appli
Sequence 57, Appl
Sequence 29, Appl
Sequence 69, Appl
Sequence 92, Appl
Sequence 92, Appl
Sequence 157, App
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Sequence 1, Appl
Sequence 2, Appl
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; Sequence 149, Application US/08222177A
; Patent No. 5582979
                                                    US-08-222-177A-149
   Query Match
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                                                                    MOLECULE TYPE: DI
IMMEDIATE SOURCE:
CLONE: mfd33rs
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LENGTH: 56 base pairs
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                     TOPOLOGY:
                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: doub
                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 53717-1914
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Sequence 1, Appli	Sequence 5, Appl1	Sequence 5, Appli	Sequence 20, Appl	Sequence 5, Appli	Sequence 114, App	Sequence 9, Appli	Sequence 40, Appl	Sequence 2, Appli	Sequence 53, Appl	Sequence 2, Appli	Sequence 4, Appli	Sequence 10, Appl	Sequence 1, Appl1	Sequence 175, App		Sequence 2, Appli	Sequence 13, Appl	Sequence 12, Appl

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GENERAL INFORMATION:
APPLICANT: Webbr, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES
NUMBER OF SEQUENCES: 460
APPLICATION NUMBER: US 07/341
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 0986
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
TELEFAX: (608) 831-2106
                                                                                                                                                                                                                                                                               COMDUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION NUMBER: US/08/222,177A
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION Release #1.0, Version #1.25
CURENT APPLICATION NATA:
APPLICATION NUMBER: US/08/469,802B
FILING DATE: 06-UN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mueting, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 31,977
REFERENCE/DOCKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 43; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 5741645
TITLE OF INVENTION: Type 1 and Method for Diagnosis NUMBER OF SEQUENCES: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 48; Conser
                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 612-305-1225
INFORMATION FOR SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Orr, Harry T.
APPLICANT: Ranum, Laura P.W.
APPLICANT: Chung, Ming-yi
APPLICANT: Zoghbi, Huda Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
sent No. 5741645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 54 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 119 No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
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b. 5741645
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                                                                                                                                                                               5, Application US/08267803B
5834183
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                                                           Ranum, Laura P.W.
Chung, Ming-yi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.2%; Score 43; DB 2; I ilarity 100.0%; Pred. No. 1.6e-06; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                       Harry T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Pred. No. 2.7e-08; ative 0; Mismatches 0; Indels
Gene Sequence for Spinocerebellar Ataxia
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MEDIUM TYPE: Floppy disk
COMPOTERS: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/267,803B
FILING DATE: 28-UN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 110.00030120
TELEPHONE: 612-305-1217
TELEPHONE: 612-305-1217
TELEPHONE: 612-305-1217
INFORMATION FOR SEO ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 54 base pairs
TYPE: nucleic acid.
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TOPOLOGY: linear;
MOLECULE TYPE: DNA
US-08-267-803B-45
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US-08-222-177A-86/c
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TITLE OF INVENTION: TY
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 86, Application US/08222177A
Patent No. 5582979
GENERAL INFORMATION:
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Best Local Similarity
Matches 43; Conserv
                                                                                                                                                                        CITY: Madison

CONTRY: Wisconsin

COUNTRY: USA
ZIP: 53717-1914

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Weber, James L.

TITLE OF INVENTION: LENGTH POLYMORPHISMS IN

TITLE OF INVENTION: (dc-da)n.(dg-dT)n SEQUENCES AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 460
CORRESPONDENCE ADDRESS:
ADDRESSEE: DeWitt Ross & Stevens, S.C.
STREET: 8000 Excelsior Drive, Suite 401
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: P.O. Box CITY: Minneapolis
STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Mueting, Raasch, Gebhardt & Schwappach, P.A. STREET: P.O. Box 581415
                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 55458-1415
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                                                                                                                                                                                                           Release #1.0, Version #1.25
                                                                                                                                                      US/08/222,177A
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; IMMEDIATE SOURCE:
; CLONE: mfdl2rs
US-08-222-177A-86
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                                                    ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 017957-000410
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEPHONE: (415) 326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 39 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Applic Patent No. 5712098
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SEQUENCE CHARACTERISTICS:
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APPLICANT:
APPLICANT;
APPLICANT;
APPLICANT:
                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/632,673B
FILING DATE: 16-APR-1996
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
TELEPAX: (608) 831-2106
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wolff, Roger K. APPLICANT: Feder, John N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: Sara, Charles S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39
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STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                       STRANDEDNESS:
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                                    nucleic acid
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Thomas, Winston J.
Drayna, Dennis T.
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DIAGNOSTIC METHODS
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L00.0%; Pred. No.
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US-08-454-557C-57/c
Sequence 57, Application US/08454557C
Parant No. 5830670
US-08-340-426D-57/c; Sequence 57, Application US/08340426D; Patent No. 5948634; GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne; APPLICANT: Wands, Jack R.
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                                                                                                                                                                                                         OY 12897 GGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGC 12934
                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (202) J. TELEFAX: (202) J. TELEFAX: (202) J. TELEFAX: FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
SEQUENCE 60 base pairs
SEQUENCE 100 base pairs
                                                                                                                                                                                                                                           Best Local
Matches 3
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Best Local Similarity
Matches 39; Conserv
                                                                                                                                                                                                                                                                                Query Match
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,557C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: de la Monte, S
APPLICANT: Wands, Jack R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16299 CCTGGGTGCTCCACCTGGCACGTATATCTCTGCTCTTCC 16337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid STRANDEDNESS: both TOPOLOGY: both
                                                                                                                                                                      CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39 CCTGGGTGCTCCACCTGGCACGTATATCTCTGCTCTTCC 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Ludwig, Steven R. REGISTRATION NUMBER: 36,203
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38; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (202) 371-2540
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                                                                                                                                                                                                                                           0.2%; Score 38; DB 3; Locality 100.0%; Pred. No. 9.2e-05; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 4.3e-4
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                                                                                                                                                                                                                                                                              Length 60;
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Gaps

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CORRESPONDENCE ADDRESS:

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US-08-450-673C-57/c
; Sequence 57, Application US/08450673C
; Patent No. 5948888
                   COUNTRY: U.S.A.
ZIP: 2005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/450,673C
FILING DATE: 30-MAY-1995
CTLASSIFICATION: 1NFORMATION:
NAME: Ludwig, Steven R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELECHIONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                         INDERAL INFORMATION:

APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.

APPLICANT: Wands, Jack R.

TITLE OF INVENTION: Of Alzheimer's Disease

TITLE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION UNMEER: US/08/340,425D
FILLING DATE: 14-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease NUMBER OF SEQUENCES: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, Suite 600 CITY: Washington STATE: D.C.
  NAME: Ludwig, Steven R. REGISTRATION NUMBER: 36,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . Match . O.2%; Score 38; DB 4; Local Similarity 100.0%; Pred. No. 9.2e-05; Local Similarity 100.0%; Pred. No. 9.2e-05; es 38; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                5: Sterne, Kessler, Goldstein & Fox P.L.L.C 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0609.3840002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT-US95-17111A-57/c; Sequence 57, Applicat; GENERAL INFORMATION:
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                                                                                                                                                                                               CT-US95-17111A-57
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                                                                Query Match
Best Local Similarity 100.
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Best Local Similarity
Matches 38; Conserv
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TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12897 GGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGC 12934
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340
FILING DATE: 14-NOV-1994
ATTORNEY/ACENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 60 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17111A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: de la Monte, Suzanne
APPLICANT: Mands, Jack R.
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression
TITLE OF INVENTION: Detection of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                     LENGTH: 60 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48 GGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGC 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: bo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A. ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1100 New CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (202)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.2%; Score 38; DB 4; I
100.0%; Pred. No. 9.2e-05;
ative 0; Mismatches 0;
                                                                                  0.2%; score 38; DB 6; Lv
100.0%; Pred. No. 9.2e-05;
ative 0; Mismatches 0;
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                                                                                                                               Length 60;
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                                                                                       Gaps
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US-08-340-426D-57

LENGTH: 60 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both

TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:

Query Match Best Local S Matches 38

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NUMBER OF SEQUENCES: I

ADDRESSEE:

STREET: 1100 New CITY: Washington STATE: D.C.

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; MOLECULE TYPE: US-08-469-802B-29
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TITLE OF INVENTION: Type 1 and Method for Diagnosis NUMBER OF SEQUENCES: 47
                                                                    Patent No. 5
                                                                                                                                                                                                        Patent No. 583418
                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 29
                                                                                                                                                                                                                             Sequence 47,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 612-305-1225
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/469,802B
FILING DATE: 06-UN-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                   APPLICANT: Ranum, Laura P.W.
APPLICANT: Chung, Ming-yi
APPLICANT: Zoghbi, Huda Y.
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
ent No. 5834183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
ent No. 5741645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                    TITLE OF INVENTION: Type 1 and Method for Diagnosis NUMBER OF SEQUENCES: 85
                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                        29
                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Mueting, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CENGTH:
                                                                                                                                                                                                                                                                                                                      GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
                                                                                                                                                                                                                       Application US/08267803B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Mueting, Raasch, Gebhardt & Schwappach, 119 No. 5741645th Fourth Street, Suite 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ranum, Laura P.W.
Chung, Ming-yi
Zoghbi, Huda Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Orr, Harry T.
                                                                                                                                                                             Orr, Harry T.
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Mueting, Raasch, Gebhardt & Schwappach, P.A.
D. Box 581415
                                                                                                                                                                                                                                                                                                                                                                                                            0.2%;
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. 9.1e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Length 66
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TELEFAX: 612-305-1228
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 base pairs
                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,557C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.2%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 69, Application US/08454557C Patent No. 5830670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
INFORMATION FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7513 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 7550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
                                     TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: de la Monte, S
APPLICANT: Wands, Jack R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                  STREET: 1100 New CITY: Washington STATE: D.C.
                                                                          REGISTRATION NUMBER: 36,203 REFERENCE/DOCKET NUMBER: 0609.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Minneapolis STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 36,602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/0 FILING DATE: 28-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 55458-1415
                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
DEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McCormack, Myra
                                                                                                             udwig, Steven R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Suzanne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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Pred. No.
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                                                                              .3840003
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. 9.1e-05;
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us-08-852-495c-1_copy_25000_45000.rni

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COMPUTER READABLE FORM:

MEDLING TYPE: Floppy disk
COMPUTER: LBM PC compatible
COMPUTER: DAY PC COMPATIBLE
COMPUTER: PACHITIA PC-DOS/MS-DOS
SOFTWARE: PACHITIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,426D
FILING DATE: 14-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: LUDWING, Steven R.
REGISTRATION NUMBER: 06.09.3840002
REFERENCE/DOCKET NUMBER: 06.09.3840002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
INFORMATION FOR SEG ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 76 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                  LENGTH: 76 base pairs;
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
US-08-340-425D-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 76 base pairs
TYPE: nucleate acid
STRANDENNESS: both
TOPOLOGY: both
US-08-454-557C-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OY 12897 GGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGC 12934
Db 48 GGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGC 11
RESULT 14
US-08-450-673C-69/c
; Sequence 69, Application US/08450673C
; Patent No. 5948888
; GENERAL INFORMATION:
                                                                                                                                                       OY 12897 GGTGAAACCCTGTCTGTCTACTAAAATACAAAATTAGC 12934
Db 48 GGTGAAACCCTGTCTCTACTAAAAATACAAAAATTAGC 11
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US-08-340-426D-69/c
                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 69, Application US/08340426D Patent No. 5948634
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL TRANT: de la Monte, Suzanne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1100 New CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Sterne, Kessler, Goldstein & Fox P.L.L.C
1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                  0.2%; Score 38; DB 4; Lilarity 100.0%; Pred. No. 8.9e-05; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 76;
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OY 12897 GGTGADACCCTGTCTCTACTADADATACADADATTAGC 12934
Db 48 GGTGADACCCTGTCTCTACTADADATACADADATTAGC 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
PCT-US95-17111A-69/c
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ATTORNEY/AGENT INFORMATION:
NAME: LUDDING STEVEN BROWN BROW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 69, Application PC/TUS9517111A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 0.2
Best Local Similarity 100.
Matches 38; Conservative
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ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION Release #1.0, V
CURRENT APPLICATION NUMBER: US/08/450,6730
FILING DATE: 30-MAY-1995
CIRCETTCATTON: SAY-1995
                                                                                                                                                     COMPUTER READABLE FORM:
MEDIJIM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA
APPLICATION NUMBER: PCT/US95/17111A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and
TITLE OF INVENTION: Detection of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1100 New
CITY: Washington
                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C
STREET: 1100 New York Avenue, Suite 600
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100.0%; Pred. No. 8.9e-05;
htive 0; Mismatches 0;
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08/340,426

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FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: LUMVIG, Steven R.
REGISTRATION NUMBER: 36,203
REGISTRATION NUMBER: 36,009.3840002
TELECOMMUNICATION INFORMATION:
TELEPHAN: (202) 371-2600
TELEPHAN: (202) 371-2540
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 76 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
PCT-US95-17111A-69
                                                                                                   Search completed: March 29, 2000, 17:48:08 Job time: 50350 sec
                                                                                                                                                                                      Query Match 0.2%; Score 38; DB 6; Length 76; Best Local Similarity 100.0%; Pred. No. 8.9e-05; Matches 38; Conservative 0; Mismatches 0; Indels
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Title:
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Maximum DB seq length: 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
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     US-08-852-495C-1_COPY_25000_45000
20001
1 AGTGCAGTAGCTGCGACCTGC
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13787.907 Million cell updates/sec
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Gapop 60.0 , Gapext 60.0
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em_est7:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

c 1	Result
51	No. Score Match Length DB ID
0.3	Query Match
70	Length
25	B .
70 25 N84707	esult Query No. Score Match Length DB ID Description
N84707 J0579F Huma	Description

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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                        REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                              RESULT
N84707/c
LOCUS
                                                                                                           COMMENT
                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNAs from fetal heart (1996)
Unpublished (1996)
Contact: Liew CC
Department of Laboratory Medicine and Pathobiology
University of Toronto
Banting Institute, 100 College St., Toronto, Ontar.
Tel: 4169788758
Fax: 4169788758
Fax: 41697887560
Email: liewcc@utcc.utoronto.ca
                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                   N84707 70 bp mF
J0579F Human fetal heart,
clone J0579 5' similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                    N84707.1
                                                                                                                                                                (bases 1 to 70)
   il: liewcc@utcc.utoronto.ca
primer: GAAATTAACCCTCACTAAAGGG
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D448088
R67088
W74145
AA555145
AQ319270
AA6114379
AA1349123
AA1832832
AA280198
B80126
AA578467
AA3756377
AA3583277
AA3583697
                                                                                                                                                                                                                                                                                                                  mRNA
                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                 RNA EST 01-APR-1996
Lambda ZAP Express Homo sapiens cDNA
REPETITIVE ELEMENT ALU, mRNA sequence.
                                                               Toronto, Ontario,
                                                                                                                                                                                                                                                                                                                                                                                                                               AQ535244 RPCI-113
B48088 RPCIII-4N6.
D44637 HUNSUPY05
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H67549 Y068110.sl
AQ319270 RPCIII-98
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AA715247 cn15d10.y
AA349123 tc51908 c
AA611479 np46c03 7H12D08 c
AA611479 np46c03 7H12D08 c
AA611479 np46c03 7H12D08 c
AA611479 np46c03 7H12D08 c
AA61198 Z104b12 r
B6016 CIT-H5-204
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AA601114 n015f06.s
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AA705667 x
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AA7047857 nx51f0.s
AA611142 nn58f10.s
AA611712 mn58f10.s
AA61712 mn58f10.s
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AUTHORS
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SOURCE
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ORIGIN
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AA082835
                                                                                                                                                                                 FEATURES
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Best Local S
Matches 51
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                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA082835 59 bp mRNA
zn21g12.s1 Stratagene neuroepithelium
cDNA clone IMAGE:548134 3' similar to
element; mRNA sequence.
AA082835 AA082835.1 GI:1624910
EST.
                                                                                                                                                                                                                                                    Generation and analysis of 280,000 human expressed sequenc genome Res. 6 (9), 807-828 (1996) 97044478 on Sep 12, 1996 this sequence version replaced gi:1404580. Contact: Wilson RK ty School of Medicine Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukherja; Prinates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 59)

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Le, N., Le, N., Le, M., Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 0.3%; Solution 0.3%; Solution 0.0%; 1 Similarity 100.0%; 1 S1; Conservative 0;
                                                                                                                                                                         Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40M13 fwd. from Amersham.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism-"Homo sapiens"
/db_xref-"taxon:9606"
/clone-"10579"
/clone-"105-79"
/clone-"105-79"
/lab_host-"E. col1 X11-Blue"
/lab_host-"E. col1 X11-Blue"
/lab_host-"E. col2 x11-Blue"
/lab_host-"E. col4 x11-Blue
/lab_host-"E. col4 x11-Blue
/lab_host-"Yestor: Lambda ZAP Express;
/lab_host-"Site-1: EcoRI adaptors were ligated, followed by digestion with Xho1, for directional cloning into predigested lambda ZAP Express."

24 a 18 c 15 g 13 t
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/clone_lib="Stratagene neuroepithelium NT2RAMI 937234"
/dev_Stage="Ntera-2/RA-MI neuroepithelial cells"
/lab_host="SOIR (Kanamycin resistant)"
/note="Yector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dT. NT2
(Ntera-2/cl.Dl) precursor cells induced with Retinoic
(Ntera-2/cl.Dl) precursor cells induced with Retinoic
Acid for 1 week, followed by 3 weeks in mitotic inhibitors
                                                                                                      /organism-"Homo sapiens"
/db_xref="GDB:3926650"
/db_xref="taxon:9606"
/clone="IMAGE:548134"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. .70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 51; DB Pred. No. 8.40
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. 8.4e-07;
ches 0;
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NT2RAMI 937234 Homo sapiens
contains Alu repetitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 70;
                                                                                                                                                                                                                                                                                                                                                                        expressed sequence
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KEYWORDS
SOURCE
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AUTHORS
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AI914923
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                                        18759
                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
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Local Similarity 100.08;
hes 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13
    4
TTTTTTTTTTTTTTTTTTTTTTTTTTGAGACAGAGTCTCACTCT 18805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 72)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AI914923 72 bp mRNA EST 28-JUL-1999 tr27e08.xl NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219558 similar to contains Alu repetitive element;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On May 1, 1997 this sequence version replaced gi:2059395 Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similar to
AI914923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: -400P from Gibco
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tissue Procurement: Chri
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1997)
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                                                                                                Similarity
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                                                                               Conservative
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                                                                                                                                                                                              /note-"Organ: ovary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.35 kb. Tumor types include: mixed mullerian tumor, papillary serous, clear cell, spindle cell. All are primary tumors, metastasis positive. Life Technologies catalog #: 11534-013"
                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_wref="taxon:9606"
/clone="IMAGE:2219558"
/clone_1ib="NCI_CGAP_Ov23"
/clone_type="tumor, 5 pooled (see description)"
/lab_host="DH10B"
                                                                                                0.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Christopher Moskaluk, M.D., Ph.D., Michael
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Pred. No.
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Pred. No.
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2e-05;
                                                                                                DB 62; 1
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                                                                                                                  Length 72
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RESULT 5
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AQ535244
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ORIGIN
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AUTHORS
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                                                                                                                                                          CEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 0.2%; Score 44; DB 104; Best Local Similarity 100.0%; Pred. No. 0.00015; Matches 44; Conservative 0; Mismatches 0;
                          AUTHORS
                                                                                                               ORGANISM
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 102)
Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K.,
Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pleter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq_primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850 Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ535244 103 bp DNA GSS 18-
RPCI-11-317H22.TV RPCI-11 Homo sapiens genomic clone
RPCI-11-317H22, genomic survey sequence.
                                                                                                                                                                                                                                               B48088 102 bp DN/
RPCI11-4N6.TP RPCI-11 Homo
                                                                                                                                                            SSD
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                                                                                                                                                                                                    genomic survey sequence. B48088
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1 (bases 1 to 103)

Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P.
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AQ535244.1 GI:4846934
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Unpublished (1997)
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                                                                                                                                        numan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="GDB:7621533"
/db_xref="taxon:9606"
/clone="RPCI-11-317H22"
                                                                                                                                                                                GI:2600325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="RPCI-11"
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clone RPCI-11-4N6,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103;
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      Jong, P. and
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Best Local :
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Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pleter de Jong
lpieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
seq primer: SP6
Class: BAC ends.
                                                                                                                         On May 5, 1995 this sequence version replaced g1:798369.
Contact: Shinji Haddano
Japan Science and Technology Corporation, NeuroGenes Project,
Univ. of Tokai School of Med.
Bohseidai, Isehara,
Tel: 81-463-91-5095
Tel: 81-463-91-5095
Tes: 81-463-91-4993
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                        cDNA clones derived from 1 Mb of the Huntington's disease locus DNA Res. 3 (4), 239-255 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                       Transcript map of the human chromosome 4p16.3 consisting of 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hadano, S., Ishida, Y., Tomiyasu, H., Yamamoto, K., Bates, G.P. and Ikeda, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 68)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D44637.1 GI:1572112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D44637 68 bp
HUMSUPY036 Human brain
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Wenter, J.C.

Use of BAC End Sequences for Sequence-Ready Map Building
Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.2%; Score 43; ilarity 100.0%; Pred. No. Conservative 0; Mismatc)
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1. .os
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cell_type="Lymphocytes"
/note="Vector: pBACe3.5; Site_1: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
24 c 25 g 21 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
/clone="RPCI-11-4N6"
/clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="GDB:7501469"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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cDNA Homo sapiens
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0.00033;
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s cDNA clone 033-00-1, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 102;
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Best Local
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y130h05.sl Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:140793 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The WashU-Merck EST Project
Unpublished (1995)
On Apr 5, 1995 this sequence version replaced g1:760768
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarriini; Hominidae; Homo.

1 (bases 1 to 96)

1 (bases 1 to 96)

1 (bases 1, c) 91)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Tansaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: F
High quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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Fax: 314 286 1810
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40; Conservative
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                             / Gev_stage="placenta obtained at birth (full term)"
//lab_host="PHIOB (ampicillin resistant)"
//lacenta; Vector: pHITOB (Pharmacia) with a full resistant (Pharmacia) (Pharmacia) (Phiotographic Vector)
//lacentalin resistant res
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/clone="033-00-1"
/clone_1ib="Human brain cDNA"
/clone_type="brain"
/tissue_type="brain"
16 c 25 g 13 t
                                                                                                                                                                                                                                                                                                                                                                                             /sex-"Female"
                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:140793"
/clone_lib="Soares placenta Nb2HP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Homo sapiens"
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Location/Qualifiers
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Pred. No.
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RESULT
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Best Local S
Matches 40
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Best Local :
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                                                                                                                                                                                                  39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chiasoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
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1 (bases 1 to 100)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Putative full length read
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Apr 14, 1993 this sequence version replaced gi:315343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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llarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                        /Clone_lib="Pancreatic Islet"
//Lisue_type="pancreatic islet"
//Lisue_type="pancreatic islet"
//Lab_host="Sour cells (kanamycin resistant)"
//Lab_host="Sour cells (kanamycin resistant)"
//Lab_host="Sourceatic Vector: pBluescript SK-; Site_1:
//Lab_host="Sourceatic PBlue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
/clone="IMAGE:339537"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="GDB:1264911"
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Pred. No.
                                                                                                                                                                                                                          Score 39;
Pred. No.
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. 0.0035;
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0.0074;
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H67549.1
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Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Rodrigo F.
Chuaqui, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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AA555145
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 98)
                                                                                                                                                                                                                                     H67549 98 bp mRNA EST 11-DEC-1995 yu68f10.sl Welzmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:238987 3' similar to contains Alu repetitive element; contains
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High quality sequence stop: 84.
Location/Qualifiers
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On Sep 12, 1996 this sequence version
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                              GI:1114431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="normal prostatic epithelial cells"
/lab_host="DH10B"
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/clone_lib="NCI_CGAP_Prll"
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/db_xref="taxon:9606"
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100.0%; Pred. No.
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Generation and analysis of 280,000 human expressed sequence tags on oct 18, 1995 this sequence version replaced gi:1026289. Contact: Wilson RK Washington University School of Medicine 4444 Forest Park parkway, Box 8501, St. Louis, MO 63108
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 102)

Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C. Use of human BAC End Sequences for Sequence-Ready Map Building Unpublished (1998)

Other_GSSS: RPCIl1-98B22.TV

Contact: Shaying Zhao, William Nierman, Mark Adams

Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                    AQ319270 102 bp DNA GSS 06-MAY-1999 RPCI-11-98B22,TJ RPCI-11 Homo sapiens genomic clone RPCI-11-98B22,
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Insert Size: 174
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Fax: 314 286 1810
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/dev_stage="35 year old"
/dev_stage="35 year old"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: nose; Vector: pBluescript SR:; Site_1:
ccorl; Site_2: XhoI; Cloned unidirectionally. Primer:
oligo dT: Olfactory epithelium, normal. Average insert
size: 0.8 kb; Uni-ZAP XR Vector. Library constructed by N.
walker, D. Lancet, Weizmann Institute of Science. -5'
adaptor sequence: 5' GAATTCGGCACGAG 3' -3' adaptor
sequence: 5' CTGCAGGTTTTTTTTTTTTTTTT 3'"
a 39 c 23 g 17 t
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100.0%; Pred. No.
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91 CCACCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGG 54
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E 1 (bases 1 to 104)

NCI-CGAP http://www.ncbi.nlm.nlh.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
On May 5, 1995 this sequence version replaced gi:798056.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R
Emmert-Buck, M.D., Ph.D.
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Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (lifo@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html seg primer: SP6 class: BAC ends.
                                                                              Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 52. Location/Qualifiers
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                                                                                                                                                                                                                  cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                            www-bio.llnl.gov/bbrp/image/image.html
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/db_xref="cDB:/537293"
/db_xref="taxon:9606"
/clone="RPCI-11"98B22"
/clone_lib="RPCI-11"
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/cell_type="Lymphocytes"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
28 c 31 g 17 t
      /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.2%; but
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                        Michael R.
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BASE COUNT
ORIGIN
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VERSION
KEYWORDS
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AI752407/c
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ORIGIN
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ORGANISM
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
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  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8635 CCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTG 8672
                                                                                                                                                                                                                                                                                        source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGGCGTG 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38; Conservative
                                                                                                                                                                                                                                                                                                       DNA Sequencing and analyses by National Institutes of Health Intramural Sequencing Center (NISC).

Plate: 15 row: d column: 10

Seq primer: M13RP1 reverse primer (ABI).

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Medical Genetics Branch
National Human Genome Research Institute
10/10C101, 9000 Rockville Pike, Bethesda,
Tel: 301-402-4877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1997)
On Dec 20, 1995 this sequence version replaced gi:1130959.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jia,L.B., Young,M.F., Touchman,J.W., Bouffard,G.G., Beckstrom-Sternberg,S.M., Green,E.D., Powell,J.I., Robey,P.G., Hotchkiss,R.N. and Francomano,C.A. SGAP: The Skeletal Genome Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 105)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone NHTBC_cn15d10 random, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cn15d10.y1 Normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AI752407
                                                                                                                                                                                                                                                                                                                                                                                                                                     Fax: 301-496-7157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Libin Jia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                   34
                                                                                                                                                                                                                                                                                                                                                                                                                : libin@helix.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:1129348"
/clone_lib="NCI_CGAP_Br1.1"
/sex="female, pooled"
/tissue_type="breast"
/lab_host="breast"
/lab_host="breast"
/lab_host="breast"
/note="vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from pooled bulk
breast tumor tissue, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. Library is not normalized. (The normalized
version of this library is NCI_CGAP_BT2.) Library was
constructed by Bento Soares and M. Fatima Bonaldo. "
19 a 26 c 29 g 30 t
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                                                                             /note="Organ:
22 c
                                                                                                                     /tissue_type="Bone"
/cell_type="Trabecular Bone Cells"
/lab_host="SURE"
                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NHTBC_cn15d10"
                                                                                                                                                                                      /sex="Female
                                                                                                                                                                                                       /clone_lib="Normal Human Trabecular Bone Cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GI:5130671
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  0.2%;
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Human Trabecular Bone Cells Homo sapiens cDNA
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  Score
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  38;
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  BB
  51;
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  Length 105;
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JOURNAL COMMENT
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AUTHORS
TITLE
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AI349123/c
LOCUS
                                 ACCESSION
VERSION
KEYWORDS
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ORGANISM
                                                                                                                                              RESULT 15
AA078003/c
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ORIGIN
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Best Local
                                                                                                                                                                                                                                                             18764 TTTTTTTTTTTTTTTTTTTTTGAGACAGAGTCTC 18800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8646 TCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCACGC 8683
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                                                                                                                                                                                                                        62 TTTTTTTTTTTTTTTTTTTTTTGAGACAGAGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
EDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: I.M.A.G.E. Consortium,
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                      AA078003 105 bp mF
7H12D08 Chromosome 7 HeLa
7H12D08, mRNA sequence.
AA078003
                                                                                                                                                                                                                                                                                                37; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 72)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                     AA078003.1 GI:1837477
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seq primer: -40UP from Gibco.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI349123.1 GI:4086329
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AI349123 72 bp mRNA EST 30-DEC-1998 ta51908.x2 NCI_CGAP_Lu25 Homo sapiens cDNA clone IMAGE:2047646 3',
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                 þ
                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="DH10B"
/note="Organ: lung; Vector: pAMP1; mRNA made from lung /note="Organ: lung; Vector: pAMP1; mRNA made from lung carcinoma tissue, cDNA made by oligo-dT priming.
Directionally cloned. Size-selected on agarose gel, average insert size 500 bp. Primary library, non-amplified. "

non-amplified. "
7 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:2047646"
/clone_11b="NCI_CGAP_Lu25"
/tissue_type="bronchioalveolar carcinoma"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
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) Mismatches
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La cDNA Library
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information
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IS CDNA Clone
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on can be
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OM nucleic - nucleic search, using sw model

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

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Result Total number of hits satisfying chosen parameters: Scoring table: Sequence: Post-processing: Listing first 45 Maximum Word size Perfect score: 0000 0000 o o O 0 0 B B Score No. is the number of results predicted by chance to have a
re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution. seq length: 8 length: 105 Query Match OLIGO_NUC , Gapop 60.0 , US-08-852-495C-1_COPY_40000_70000 30001 311585 seqs, 125096042 residues March 29, 2000, 17:55:02; GTGTCACTCACGTTCAGCTA.....AACAACAGTTGCAGAATTGA 30001 Length B Gapext 60. T88080 Q66922 V27940 Q33621 Q33621 summaries Search time 599.46 Seconds (without alignments) 12521.290 Million cell updates/sec Human secreted pro 3' portion of cDNA Poly-dA 50mer prob Human GalR3 primer Lelystad virus pri Human secreted pro 3' portion of cDNA Nucleotide sequenc Analytical solid p Nucleotide sequenc Alu PCR primer 2. Trypsin inhibitory Polyester coding s psport-ic syntheti Microsatellite seq Microsatellite seq Microsatellite s Microsatellite s Oligonucleotide Oligonucleotide sp Nucleotide sequenc Human secreted pro Homo sapiens clone Porcine reproducti Sequence of oligo Sequence of oligo DNA molecule encod Human mitochondria Sequence of a micr Human chondromodul

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prolymorphic bovine DNA markers - used in genetic identification, or Polymorphic bovine DNA markers - used in genetic identification, gene mappling, and selective breeding a Table 7; Page 271; 517pp; English.

The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine Mbol DNA fragments of between 250 and 500 bp with an (Ac)15 and a (Tc)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and Mbol sites, the frequency of (76)n >9 microsatellites in the bovine genome is estimated at >100, DNA fragments of the sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence amplification of the corresp. microsatellite (using the program of DTIPRIM). The microsatellites may be used to identify individuals, cf or parentage testing, and in the genetic mapping of economic trait cross-testing, and in the genetic mapping of economic trait craits esp. in cattle, to allow selective breeding.

See also 033501-34437.

Seguence 444 BP; 22 A; 0 C; 0 G; 22 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 43; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Replication initiator protein complex - comprises 60 and 100 kD fractions for diagnosis, treatment and prevention of sepsis, viral infection and cancer. Example 2; Page 42; B2pp; English. Competition experiments using the DNAseI protection assay showed that an oligonucleotide contg. 15 tandem ATT repeats was an effective competitor for binding of the HeLa factor. This oligo was used to prepare an oligonucleotide affinity column for purification of RIP60 from Chinese hamster cells. The protein recognises and binds to an (ATT)n motif in the diff gene ori. It can also bind to the yeast ARSI domain B. See Q22753 and Q24811.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-AUG-1992.
15-JAN-1992;
15-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonucleotide containing RIP60 binding motif (ATT)15.
Dihydrofolate reductase; stably bent DNA; RIP60; RIP100; helicase;
DNA footprinting; (ATT)n binding factor; yeast ARS1;
oligonucleotide affinity column; ss.
                                                                                                                                                                                                        (UYRO) ROCKEFELLER UNIV.
(UYVE) UNIV OF VERMONT.
Heintz N, Heintz NH, Dailey LA, Caddle MS;
WPI; 92-096839/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Georges M, Massey JM;
WPI; 92-284684/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.1%;
llarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                        9. .11
/*tag= b
/note= "RIP60 binding motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
9. .53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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RESULT Q71814 ID Q7 AC Q7 DT 3(DE PC

071814 standard; DNA; 81 BP.
071814;
30-MAR-1995 (first entry)
Polyester coding sequence for insertion into

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μ.

AATAATAATAATAATAATAATAATAATAATAATAATAA 41

Query Match
Best Local Similarity
Matches 41; Conser

Conservative

0;

0.1%;

Score 41; DB Pred. No. 0.0 0; Mismatches

DB 1; 0.0038; 0,

Length 80

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PI Gruskin EA;

Why 1; 94-773234/34.

PT New biocompatible medical devices and articles - using a lactic process.

PT scid-glycolic acid polyester in which monomer units are processed and specifically determined sequence represents the 5' fragment of the synthetic genes which cannot polyesters given in 071801-02. This fragment was ligated into cende polyesters given in 071801-02. This fragment was ligated into cand 5' ends of the plasmid psporT in digested with FokI. This places cand 5' ends of the plasmid psporT in digested with FokI. This places cand 5' ends of the plasmid psporT in digested with FokI. This places can 5' ends of the plasmid psporT in digested with FokI. This places can 5' ends of the plasmid psporT in digested with FokI. This places can in 071801-02 in an E. coli cell free medium. The expressed can sequences represent synthetic genes which were used in the synthesis complete the coli trap initiator.

CC of polyesters derived from the amaino acid analogues of an amino acid except pro. of the three stop codons, UAA, UAG and UGA, one of these coli call trap and UAA, one of these coli call trap and UAA, one of these cannot can be polyester. Lactate and glycolate are encoded by UAA and CC UAG, respectively. Initiation of translation may be encoded by an accomplished through the use of a specially modified to carry lactate instead of Met alternatively, a Met is incorporated in the first position of the polymer chain. The cc resulting polymer is treated with cyanogen bromide to remove the Met. CC opolymers produced in this manner may be used to produce sutures, so sequence 80 Bp; 47 A; 6 C; 4 G; 23 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
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Best Local S
Matches 41
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CA2112716-A.
01-JUL-1994.
11-DEC-1993; 112716.
31-DEC-1992; US-99520.
(USSU ) US SURGICAL CORP.
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Q71808 standard; DNA; 80 BP.
Q71808 standard; DNA; 80 BP.
Q71808.
Q71808:

Q71808
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llarity 100.0%;
Conservative
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 u
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0.0041;
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31-DEC-1993; 112716.
31-DEC-1992; US-999520.
(USSU) US SURGICAL CORP.
Gruskin EA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27146 AATAATAATAATAATAATAATAATAATAATAATAATAA 27186
                                                                                                                                                                                                                  30-MAR-1995 (first entry)
30-MAR-1995 (first entry)
30-MAR-1995 (first entry)
pSPORT-IC synthetic polyester gene 5' fragment and trpA initiator.
Synthetic gene; synthesis; polyester; a-amino acid analogue; clips;
stop codon; stop signal; monomer unit; lactate; glycolate; staples;
stop codon; stop signal; monomer unit; lactate; glycolate; stop codon; stop signal; monomide; Met-tRNAf; cyanogen bromide; pins
translation initiation; modified; Met-tRNAf; cyanogen bromide; pins
                                                                                                                                                                                                                                                                                                                           Q71809 standard;
Q71809;
30-MAR-1995 (fi:
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                                                       misc_feature
                                                                                                                 misc_feature
                                                                                                                                                                    misc_signal
                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   devices, pins and screws. Sequence 81 BP; 47 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              co-polymer;
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                                                                                                                 /note-
19. .21
                                     /note=
22. 9:
/*tag=
                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                      /*tag=
                                                           . 93
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                                                                       "Start
                                                                                                                               "trpA initiator'
                   "Polyester gene 5' fragment"
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Pred. No.
                                                                           codon
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G;
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0.0038;
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233621 DB 33621 DB 33621 DB 33621 DB 3621 DB 3
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Pri hidividually and state of the chain may be encoded by an and Componer the first lactate of the chain may be encoded by an and Componer between the first position of the polymer sproduced in this manner may be used to produce sutures, and Componer between the first position of the polymer chain. The componer of the polymer sproduced in this manner may be used to produce sutures, sequence 103 BP; 58 A; 7 C; 9 G; 29 T;
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Best Local S
Matches 41
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31-DEC-1993; 112716.
31-DEC-1992; US-99952
(USSU ) US SURGICAL C
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15-JAN-1992; 1
15-JAN-1991; 1
gene mapping, and selective breeding
Table 7; Page 178; 517p; English.
The sequence is that of a bovine microsatellite sequence obtd. by
screening a library of bovine MboI DNA fragments of between
250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.
One out of 50 clones cross hybridised. Assuming independent
distribution of microsatellites and MboI sites, the frequency of
(T6)n >9 microsatellites in the bovine genome is estimated at >100,
000. The sequence information for ca. 230 such bovine microsatellites
is summarised in the specification and indexed herein (see below).
The sequences upstream and downstream of the microsatellite sequence
                                                                                                                                                                                                                                                                                                                                                                 Georges M, Massey JM;
WPI; 92-284684/34.
Polymorphic bovine DNA markers .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus.
WO9213102-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Microsatellite sequence from clone GBFSH.
PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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02-FEB-1993 (first entry)
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                            genetic
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                                                                                                                                                                                                                                                                                                                                                                               identification
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RESULT
Q52732
ID Q5
AC Q5
DT 20
DE S6
DE as
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                                                                                                                                                                                                                                                                                                                    Pr Polymorphic bowine DNA markers - used in genetic identification, pr Polymorphic bowine DNA markers - used in genetic identification, pr gene mapphing, and selective breeding Table 7; Page 178; $17pp; English.

PS Table 7; Page 178; $17pp; English.

CC The sequence is that of a bowine microsatellite sequence obtd. by cc careening a library of bowine Mol DNA fragments of between cc careening a library of bowine Mol DNA fragments of between cc careening a library of bowine Mol DNA fragments of between cc careening a library of bowine Mol DNA fragments of between cc careening a library of bowine microsatellites in the specification and stress, the frequency of cc careening and interested at >100, cc careening and interested at >100, cc careening and commatise of setting the sequence information for ca. 230 such bowine microsatellites cits summarised in the specification and indexed herein (see below).

CC the sequences upstream and downstream of the microsatellite sequence camplification of the corresp. microsatellite (using the program cc camplification of the corresp. microsatellite (using the program cc camplification). The microsatellites are been considered trait cc. 1 coi, or genes involved the determinism of economic trait cc. traits esp. in cattle, to allow selective breeding.

Sequence 53 BP; 20 A; 0 C; 0 G; 33 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.18;
Best Local Similarity 100.08;
Matches 40; Conservative
                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                       Matches
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15-JAN-1992;
15-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         were used to generate the required PCR primers for in vitro amplification of the corresp, microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding. See also 033501-34437.

Sequence 53 BP; 20 A; 0 C; 0 G; 33 T;
052732 standard; DNA; 56 BP. 052733; 052733; 20-UNN-1994 (first entry) sequence of oligo nucleotide adaptor used for the synthesis of asymmertically tailed plasmid primers for use in cloning libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-FEB-1993 (first entry)
MicroSatellite sequence from clone GBFSH.
PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Georges M, Massey JM;
WPI; 92-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genetic mapping;
Bos taurus.
WO9213102-A.
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Q33621 standard;
Q33621;
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                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                     0.1%;
ilarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                     Score 40;
Pred. No.
                                                                                                                                                                                                                                       Mismatches
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0.0
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0.0081;
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.0081;
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RESULT 10
Q52734
ID Q52734
AC Q52734
DE Sequen
DE ASYMME
KEY
FT M1sc_f
FT M1
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Best Local Similarity
Matches 39; Conserv
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14-DEC-1993.
21-APR-1989; 341523.
21-APR-1989; US-341523.
12-AUG-1992; US-928856.
(HOFF ) HOFFFANN LA ROCHE II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US5270185-A.
14-DEC-1993.
14-DEC-1993.
21-APR-1989; 341523.
21-APR-1989; US-341523.
12-AUG-1992; US-928856.
(HOFF; ) HOFFMANN LA ROCHE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Figure 3A; 13pp; English.
Claim 4; Figure 3A; 13pp; English.
The inventors claim an asymmetrically tailed plasmid primer comprising a cut,ds DNA plasmid contg. a functional origin of replication and at least one functional selection marker gene, one 3 terminus of which contains an oligo (dT) extension, the other 3' terminus of which contains an oligo (dC) or oligo (dG) extension terminus of which contains an oligo (dC) or oligo (dG) extension terminated by a 3' phosphate group. More specifically, the asymmetrically tailed plasmid primer is produced by SacI and KpnI cleavage of plasmid plp, and each terminus produced by the cleavage is joined to the complementary adaptor, which is Q52731 or Q52732.

Sequence 56 BP; 1 A; 6 C; 8 G; 41 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Margolskee RF;
MPI; 93-404926/50.
Asymmetrically tailed plasmid primers - comprises cut,
double-stranded DNA plasmid, useful for producing cloning
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Q52734;
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Claim 5; Figure 3B; 13pp; English.
The inventors claim an asymmetrically tailed plasmid primer comprising a cut, ds DNA plasmid contg. a functional origin of replication and at least one functional selection marker gene,
                                                                                                                        wPI; 93-404926/50.
Asymmetrically tailed plasmid primers - comprises cut, double-stranded DNA plasmid, useful for producing cloning
                                                                                                                                                                                         Margolskee
WPI; 93-404
                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-JUN-1994 (first entry)
Sequence of oligo nucleotide adaptor used for the synthesis of asymmetrically tailed plasmid primers for use in cloning libraries.
Asymmetrically tailed plasmid primer; adaptor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
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ilarity 100.0%;
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Pred. No.
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RESULT
O78635
IO AC O78
AC O79
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                                                                                                                                                                                                                                                                                                    RESULT
V05740
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Matches 39
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Best Local S
Matches 39
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11-MAY-1994; 107364.
11-MAY-1993; JP-109620.
17-DEC-1993; JP-318298.
17-DEC-1993; JP-318298.
(SUZU/) SUZUKI F.
(MITU) MITSUBISHI KASEI CORP.
(MITU) KOhara A, Kondo J,
SUZUKI J, Takahashi K, Yamada E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chondrocytes and inhibits vascular endothelial cell growth care for the chondrocytes and inhibits vascular endothelial cell growth example 4; Page 10; 34pp; English.

Q78635 and Q78636 are a pair of primers for Q78627-Q78632 which encode R65486-R65491 respectively, human chondromodulin-1 (CM-1), a chondrocyte growth regulator. CM-1 as part of a pharmaceutical compsn. with a carrier, excipient or solvent, can be used to stimulate chondrocyte growth. CM-1 also inhibits vascular endothelial cell growth, by promoting the differential potency of chondrocytes.

Sequence 61 BP; 2 A; 8 C; 8 G; 43 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         terminus of which contains an oligo (dT) extension, the other 3' terminus of which contains an oligo (dC) or oligo (dG) extension terminated by a 3' phosphate group. More specifically, the plasmid primer is produced by EcoRI and HindIII cleavage of plasmid pUC19, and each terminus produced by the cleavage is joined to the complementary adaptor, which is Q52733 or Q52734. Sequence 56 BP; 1 A; 5 C; 8 G; 42 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q78635;
Q78635;
11-DEC-1997.
06-JUN-1997: U09878.
07-JUN-1996: US-659224.
(GEMY) GENETICS INST INC
                                                                                                 Homo sapiens. W09746683-A2.
                                                                                                                                                  Secreted protein; homol nutritional supplement;
                                                                                                                                                                                                Nucleotide sequence of the 3'
                                                                                                                                                                                                                                                    V05740
V05740;
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EP-624645-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chondromodulin-1; chondrocyte growth regulation; vascular endothelial cell growth; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human chondromodulin-1 cDNA pr
Chondromodulin-1; chondrocyte
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                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
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Similarity 100.0%;
39; Conservative 0;
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                                                                                                                                          ce of the 3' portion of clone AS301, homology; antibody; immunoassay rement; therapeutic activity; ds.
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Query Match Best Local S Matches 39

Similarity

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Score 39; DB Pred. No. 0.0 0; Mismatches

39; 0.08 .013;

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PT Nucleic acids encoding secreted proteins from clones within ATCC PT 98076 - useful as immuno-modulators, anti-proliferative agents, 98076 - useful as immuno-modulators, anti-proliferative agents, 98076 - useful as immuno-modulators, and tissue growth, etc PT 98076 - useful at properson and tissue growth, etc Claim 40; Page 76; 99pp; English.

CC Enaim 40; Page 76; 99pp; English.

CC Drain cone As301_2. The clone was isolated from a human fetal portion of clone As301_2. The clone was isolated from a human fetal cone conding a secreted protein. V05739 provides 5; portion of the nucleotide concoding a secreted protein. V05739 provides 5; portion of the nucleotide concoding a secreted protein. V05739 provides 5; portion of the nucleotide concoding a secreted protein. V05739 provides 5; portion of the nucleotide concoding a secreted protein. V05739 provides 5; portion of the nucleotide concoding a secreted protein. V05739 provides 5; portion of the nucleotide concoding a secreted protein of genetic disorders and sources control concoding and primers. They can also be used to generate anti-protein concoding and protein is useful for raising antibodies, as immunoassay reagents and as nutritional supplements. The protein may possibly have any of a protein and protein anti-protein and protein and protein and possibly have any of a protein and prot
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Best Local S
Matches 39
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                                            Example 7; Page 21-26; O/PP) variable. Example from the present sequence represents a probe used in an example from the present invention. The present invention describes an analytical solid phase method for detecting nucleic acids. The method comprises obtaining a base sequence which hybridises with the polynucleotide sequence of the target, and a set of probes immobilised on the solid phase via a linker which is enzymatically ligated during hybridisation. The product is used for the detection of specific nucleic acids. Possible fields of application include diagnosis of disease, detection of drug sensitivity, screening for appropriate transplantation organs, testing in the food industry to prevent food poisoning. A simple, quick method for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bowman M, E
Merberg D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-MAR-1998.
12-SEP-1997; J03232.
13-SEP-1996; JP-243720.
(MOLE-) LAB MOLECULAR BIOPHOTONICS.
Abe S, Sato Y;
Abe S, Sato Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Analytical solid phase nucleic acid detection hybridisation probe 16. Analytical solid phase; detection; hybridisation; probe; target; diagnosis; screening; disease; drug sensitivity; transplantation organifood industry; food poisoning; ss.
screening for appropriate transplantation organs, testing industry to prevent food poisoning. A simple, quick method selectively detecting target in a mixed sample is obtained sequence 90 BP; 6 A; 14 C; 13 G; 57 T;
                                                                                                                                                                                                                                                                                                                                                                         WPI; 98-271664/24.

Analytical solid phase for detecting nucleic acids - contains sequence which hybridises with polynucleotide sequence of transper, and a set of probes immobilised on the solid phase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           great variety of therapeutic activities.
Sequence 87 BP; 79 A; 4 C; 4 G;
                                                                                                                                                                                                                                                                                                                       Example 7; Page 21-22; 37pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
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llarity 100.0%;
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A, Spaulding
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Pred. No. 0.0
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.014;
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V19045
ID V19045
AC V19045
AC V19045
DE Alu PC
KW PCR: p
KW Circul
DS Saccha
CS Saccha
PN W09901
PD 15-JM
PR (USSH)
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pp 06-JUN-1995; US-659224.
pp (GEMY) GENETICS INST INC.
pr (GEMY) GENETICS INC.
pr (GEMY) GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
WO9746683-A2.
11-DEC-1997.
13-JAN-1998:
109-JUL-1996; WO-U11478.
09-JUL-1996; WO-U11478.
09-JUL-1996; WO-U11478.
CUSSH ) US DEPT HEALTH & HUMAN SERVICES.
KOUPTINA NY. Larionov VL, Perkins EL, Resnick MA;
WPI; 99-110234/L0.
Preparation of yeast artificial chromosomes - by in vivo recombination using vector comprising yeast centromere, marker, yeast telomere and nucleic acid for recombination Example 1; Page 45; 117pp; English.
This is the nucleotide sequence for the PCR primer used in the amplification of the Alu repeat sequence, which is used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                V19045;
28-JUL-1998 (first entry)
Alu PCR primer 2.
PCR; primer; amplification; Alu repeat sequence; vector;
circular yeast artificial chromosome; YAC; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUN-1998 (first entry)

Nucleotide sequence of the 3' portion from clone AJ147_1.

Secreted protein; antibody: immunoassay reagent;

nutritional supplement; therapeutic activity; murine; calmegin; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
Saccharomyces sp.
WO9801573-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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V05728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        V19045 standard; DNA; 40 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.1%; 5c.
100.0%; Pr/
''' 0;
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G;
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0.013;
hes 0; Indels
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                                                                    Query Match
Best Local S
Matches 38
                    8613 GAGGCTGAGGCAGGAGAATCGCTTGAACCCCGGGAGGCG 8650
                                                                                                                                                      demonstrate the processes described in the invention. It involves the creation and use of circular yeast artificial chromosome (YAC) to selectively clone specific nucleic acids from a background of mixed nucleic acids by introducing the vector(s) into E. coli cells. They can be used to rapidly isolate human DNA where only a part of the sequence of DNA is known. Using the methods large fragments of DNA can be easily cloned and analysed.

Sequence 40 BP; 9 A; 8 C; 19 G; 4 T;
2 GAGGCTGAGGCAGGAGATCGCTTGAACCCGGGAGGCG 39
                                                                                       Similarity
                                                                      Conservative
                                                                                       0.1%;
                                                                    0; Mismatches
                                                                                       Score 38; pred. No.
                                                                                       DB 1;
0.032;
                                                                      0;
                                                                                                        Length 40;
                                                                      Indels
                                                                      0;
                                                                      Gaps
                                                                      0
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Search completed: March 30, 2000, 00:58:13 Job time: 76091 sec



Title: Perfect score:

US-08-852-495C-1_COPY_40000_70000 30001

GTGTCACTCACGTTCAGCTA.....AACAACAGTTGCAGAATTGA 30001

March 29, 2000, 17:48:08; Search time 340.37 Seconds (without alignments)
10552.676 Million cell updates/sec

OM nucleic - nucleic search, using sw model

GenCore version 4.5 Copyright (c) 1993 - 2000 Comp

Compugen Ltd

Scoring table:

Gapop 60.0 ,

Gapext 60.0

Minimum DB seq length: 8
Maximum DB seq length: 105

Post-processing: Listing first 45

summaries

Issued_Patents_NA: *

/cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/5C_COMB.seq:*
/cgn2_6/ptodata/1/ina/5D_COMB.seq:*
/cgn2_6/ptodata/1/ina/5D_COMB.seq:*
/cgn2_6/ptodata/1/ina/pcru9S_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*

Total number of hits satisfying chosen parameters:

214294 seqs, 59861574 residues

Word size :

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COMPUTER: IBM PC COMPATIBLE

COMPUTER: IBM PC COMPATIBLE

SOFTWARE: PATENTH PC-DOS/MS-DOS

SOFTWARE: PATENTH Release #1.0, Version #1.30

CURRENT APPLICATION NOME:

APPLICATION NUMBER: US/08/632,673B

FILING DATE: 16-APR-1996

CLASSIFICATION 435

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M.

REGISTRATION NUMBER: 030,223

REFERENCE/DOCKET NUMBER: 017957-000410

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 326-2420

TELEPAX: (415) 326-2420

TELEPAX: (415) 326-2422

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 39 base pairs

TYDEF: nnc/aff acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-632-673B-1/c
US-08-632-673B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Tsuchi
           MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ruddy, David
APPLICANT: Wolff, Roger K.
APPLICANT: Feder, John N.
TITLE OF INVENTION: HEREDITARY HEMOCHROMATOSIS
TITLE OF INVENTION: DIAGNOSTIC MARKERS AND DIAGNOSTIC METHODS
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                       TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                         San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , Application US/08632673B 5712098
                                                                                                                                                                                                                                                                                                                                                                                                            USA
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Thomas, Winston J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drayna, Dennis T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tsuchihashi,
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NO
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US-08-450-673C-91
US-08-450-673C-91
US-08-450-673C-91
US-08-454-557-29
US-08-454-557-92
US-08-450-673C-92
US-08-450-673C-92
US-08-450-673C-92
US-08-450-673C-92
US-08-778-494B-114
US-08-582-562A-8
US-08-778-494B-137
US-08-859-998-1373
US-08-859-998-1373
US-08-859-998-1373
US-08-859-998-1373
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US-08-859-998-1373
US-08-859-998-1373
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92, Appl
92, Appl
10, Appl
11, Appl
11, Appl
16, Appl
16, Appl
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Result

51

greater than

greater than or equal to the score of the result being derived by analysis of the total score distribution

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Query Match

Length

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US-08-632-673B-1
US-08-241-465B-11
US-08-241-465B-12
US-08-231-565A-40
US-09-007-6944-13
US-08-776-944-13
US-08-776-24B-12
US-08-713-646A-44
US-08-113-646A-44
US-08-113-646A-41
US-08-113-646A-41
US-08-113-646A-41
US-08-113-646A-41
US-08-13-646A-41
US-08-702-344-7
US-08-702-344-7
US-08-702-344-7
US-08-664-596B-3
US-08-677-944-2
US-08-787-977-42

Sequence Sequence Sequence Sequence Sequence Sequence

1, Appl 42, Appl 40, Appl 40, Appl 10, Appl 113, Appl 13, Appl 14, Appl 14, Appl 14, Appl 17, Appl 17, Appl 18, Appl 19, Appl 19, Appl 19, Appl 19, Appl 19, Appl

Sequence Sequence Sequence

Sequence Sequence Sequence Sequence Sequence Sequence Sequence

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RESULT 2
US-08-241-465B-11
                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: Other nucleic acid, Synthetic DNA US-08-241-465B-11
                                                                                 RESULT 3
US-08-417-174-42
Sequence 42, Application US/08417174
Patent NO. 5844075
GENERAL INFORMATION:
APPLICANT: KAWAKAMI, YUTAKA; ROSENBERG,
                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEO ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 base pairs
LENGTH: 60 base pairs
INFORMEDNESS: single
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/08241465B
Patent No. 5719125
                                                                                                                                                                                                                                          Ouery Match 0.1%; Score 39; DB 2;
Best Local Similarity 100.0%; Pred. No. 0.000;
Matches 39; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                               APPLICATION NUMBER: US/08/241
FILING DATE: May 11, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WAITEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/241,465B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: HUMAN CHONDROMODULIN-I PROTEIN NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: W
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Ei YAMADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Atsuko KOHARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kazuhiro TAKAHASHI
Junko SUZUKI
Jun KONDO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yuji HIRAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fujio SUZUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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100.0%; Pred. No. 0.00033
htive 0; Mismatches 0
                                                                                                                                                                                                                                                              0.00031;
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                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                            0;
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                                                                                                                                                                                                                                            0
                                                                                                                                                                     US-08-231-565A-40
US-08-231-565A-40
US-08-231-565A-40

Sequence 40, Application US/08231565A

Patent No. 5874560

GENERAL INFORMATION:
APPLICANT: STEVEN A.

APPLICANT: STEVEN A.

APPLICANT: STEVEN A.

TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: METHODS

TITLE OF INVENTION: METHODS

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: FLOPPY DISK
COMPUTER: LBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,174
FILING DATE: 05-APR-1995
PRIOR APPLICATION NUMBER: US/08/231,565
FILING DATE: 22-APR-1994
CLASSIFICATION: 43-
APPLICATION NUMBER: 37,341
CLASSIFICATION: M. GRUPPI
REGISTRATION UNMBER: 37,341
REFERENCE/DOCKET NUMBER: 3026-4124U:
REFERENCE/DOCKET NUMBER: 3026-4124U:
TELECOMMUNICATION INFORMATION:
TELECOMSUNICATION INFORMATION:
TELECANS: (212) 758-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 58
TYPE: NUCLECTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: US-08-417-174-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.1%; Score 38; DB 3; Best Local Similarity 100.0%; Pred. No. 0.0006 Matches 38; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: STEVEN A.
TITLE OF INVENTION: MELANOMA ANTIGENS AND
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: METHODS
UNMBER OF SEQUENCES: 126
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                        COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                 STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10154
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Best Local Similarity
Matches 38. Conserv
                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/231,565
FILING DATE: 22-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4124
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/231
FILING DATE: 22-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REGISTRATION NUMBER: 2026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPHONE: (212) 751-6849
TELEPAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: DOU TOPOLOGY: UNKNOWN MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: MELANOM THEIR UNTITLE OF INVENTION: METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII
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                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U
                                             TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                              NEW YORK
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                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STEVEN A.
                                               (212) 751-6849
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100.0%; Pred. No.
tive 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THEIR USE IN DIAGNOSTIC AND THERAPEUTIC
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TYPE: NUCLEOTIDE
STRANDEDNESS: DOUBLE
TOPOLOGY: UNKNOWN
MOLECULE TYPE: CDNA
US-09-007-961-40
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                                                                                        ;
ORGANELLE:
US-08-776-944-12
                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4006
TELEPAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 38; Conserv
   Matches
                Query Match
Best Local Similarity
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                                                                                                                                       HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/776,944
FILING DATE: 14-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9417211.1
FILING DATE: 25-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: TULLY, GILLIAN
APPLICANT: SULLIVAN, KEVIN
TITLE OF INVENTION: NUCLEOTIDE SEQUENCING METHOD
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
NUTYON & VANDERHYE P.C.
                                                                                                                                                                             MOLECULE TYPE: DA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                                                         NAME: CRAWFORD, ARTHUR R. REGISTRATION NUMBER: 25,3
                                                                                                                          ORGANISM:
                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                              nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/08776944
                                                                                                                                                                                                               linear
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     Conservative
                                                                                                        Mitochondrion
                                                                                                                                                                                             DNA (genomic)
                                                                                                                                                                                                                                single
0.1%; Score 38; DB 4; L
100.0%; Pred. No. 0.00064;
ative 0; Mismatches 0;
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ER: 1498-92
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Pred. No.
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                                  Length 70;
     Indels
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ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
ORGANELLE: Mitochondrion
US-08-776-944-13
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US-07-920-281C-25/c
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US-08-776-944-13
                                                                                                                                                                                                                                                                                                                       Sequence 25, Application US/07920281C
Patent No. 5739026
GENERAL INFORMATION:
APPLICANT: Garoff, Henrik
APPLICANT: Liljestrom, Peter
TITLE OF INVENTION: DNA Expression Systems Based
TITLE OF INVENTION: Alphaviruses
NUMBER OF SEQUENCES: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/776,944
ETILING DATE: 14-FEB-1997
CLASSIFICATION: 435-1997
CLASSIFICATION: 435-1997
CLASSIFICATION: DATA:
APPLICATION NUMBER: GB 9417211.1
APPLICATION NUMBER: GB 9417211.1
FILING DATE: 25-AUG-1994
AFTORNEY/AGENT INFORMATION:
NAME: CRAWFORD, AFTHUR R:
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 1498-92
TELLECOMMUNICATION INFORMATION:
TELLEPHONE: (703) 816-4006
TELEPHONE: (703) 816-4006
TELEPAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 0.1%; Score 38; Best Local Similarity 100.0%; Pred. No. Matches 38; Conservative 0; Mismatc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SULLIVAN, KEVIN
TITLE OF INVENTION: NUCLEOTIDE SEQUENCING METHOD
NUMBER OF SEQUENCE: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE POTHETICAL: P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1100 NOR CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 75 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
    ADDRESSEE:
                                                                                                                                                                                                                                                                                     ADDRESSEE:
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59255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIXON & VANDERHYE P.C.
  Birch, Stewart, Kolasch & Birch
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                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                   0.00063;
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; LOCATION: 1.80
; OTHER INFORMATION:
; OTHER INFORMATION:
; OTHER INFORMATION:
; OTHER INFORMATION:
                                                                                                                                                                                                             Sequence 44, Application US/08113646A
Patent No. 5578468
GENERAL INFORMATION:
APPLICANT: PICKUP, David J.
APPLICANT: ANTCZAK, James B.
TITLE OF INVENTION: SITE-SPECIFIC RNA CLEAVAGE
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
US-08-113-646A-44/c
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TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mulphy 17., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 828
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
TELEFAX: 703-241-2848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM:
FEATURE:
ZIP: 2201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-005/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIF: 22040-0747
COMPUTER READABLE FORM:
COMPUTER: REPORT STORM:
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
ORGANISM: Semliki Forest Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE HYPOTHETICAL: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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                                                                                                                                   STREET: 1100 NON CITY: ARLINGTON STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                COUNTRY: U.S.A.
ZIP: 22201-4714
                                                                                                                                                                               ADDRESSEE: NIXON & VANDERHYE P.C. STREET: 1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ET: P.O. Box 747
: Falls Church
E: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.1%; Score 38; DB 2; I
ilarity 100.0%; Pred. No. 0.00062;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label- terminator
/note- "3' terminal sequence of cDNA expression
vector complementary to alphavirus genomic RNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US/07/920,281C
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US-08-771-624B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1579
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEFX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
                                                                                                       COMPUTER READABLE FORM.

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/771,624B
FILING DATE: 20-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/009,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 591423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                             STREET: L/L.
CITY: Deerfield
CTATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 0: FILING DATE: 10-AUG-1987 ATTORNEY/AGENT INFORMATION:
                                                                APPLICATION NUMBER: US 60
FILING DATE: 22-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ullman, Edwin F.
TITLE OF INVENTION: Homogeneous Amplification and Detection
TITLE OF INVENTION: of Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37
NAME: RUSZALA, LOIS K.
REGISTRATION NUMBER: 39,074
REFERENCE/DOCKET NUMBER: 10
SLECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/C
FILING DATE: 31-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37; Conservative
                                                                                                                                                                                                                                                                                                             60015-0778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/08771624B
                                                                                                                                                                                                                                                                                                                                                                             E: Behring Diagnostics GmbH, c/o Dade Behring Inc
1717 Deerfield Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rose, Samuel J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lin, Claire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patel, Rajesh D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yen Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.1%; Score 37;
100.0%; Pred. No.
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                                                                                                                                                                                                                    Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
. 0.0015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 37;
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                   JS-08-440-209-4
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US-08-440-209-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Han, Jang
APPLICANT: Spaete, R
TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08440209
Patent No. 5922857
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DAIL.
APPLICATION NUMBER: US 08/120,
APPLICATION NUMBER: 28-SEP-1993
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Janiuk, Anthony J
NAME: JANIUMBER: 29,809
                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: COTTELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (847) 267-502
TELEFAX: (847) 267-602
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL: NANTI-SENSE: NO FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FOR...

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER:
CARROLLER COMPATION NUMBER:
CARROLLER COMPAT
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE: YE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/4
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield, and Sacks P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0 FILING DATE: 12-MAY-1995 CLASSIFICATION: 435
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les 37; Conserv
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
                                                                                                      TOPOLOGY:
                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Boston
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                                                                                                                                                              nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                               linear
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47) 267-6024
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                                                                  CDNA
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                                                                                                                                single
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100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Methods and Compositions for Controlling Translation of HCV Proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08/477,895
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RESULT 13
US-08-113-646A-41/c
Sequence 41, Application US/08113646A
Patent No. 5578468
Patent No. 5578461
CENTRAL INFORMATION:
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US-08-420-443-1/c
                                                                                                                                                                                                                                             STRANDEDNESS: Sit
; TOPOLOGY: linear
US-08-420-443-1
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                                                                                                                                                                                                                                                                                                                                   Query Match 0.1%; Score 37; DB 1; Best Local Similarity 100.0%; Pred. No. 0.0014; Matches 37; Conservative 0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (617) 542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Y. ROCKY TSAO
REGISTRATION UNMEER: 34,053
REFERENCE/DOCKET NUMBER: 057
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-8906
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATE: US/07/990,298
APPLICATION UNMER: US/07/990,298
FILING DATE: 19921210
ATTORNEY/AGENT INFORMATION:
NAME: Y. ROCKY TSAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/420,443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANN: C. Bruce Bagwell
TITLE OF INVENTION: NUCLEIC ACID PROBES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
APPLICANT: ANTCZAK, James B.
TITLE OF INVENTION: SITE-SPECIFIC RNA CLEAVAGE
                  APPLICANT: PICKUP, David J.
APPLICANT: PATEL, Dhavalkumar
APPLICANT: ANTCZAK, James B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Fish
STREET: 225 Fran
CITY: Boston
STATE: Massachus
COUNTRY: U.S.A.
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
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225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ۲.
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US-08-702-344-7/c
; Sequence 7, Application US/08702344
; Patent No. 5723315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNES: WILSON, MARI.

NAME: WILSON, MARI.

REGISTRATION NUMBER: 32,955

REGISTRATION NUMBER: 1579.

TELEPOMINICATION: TOORWATION:

TELEPHONE: (703) 816-4000

TELEPA: (703) 816-4000

TELEEX: 200797 MIXIN UR

INFORMATION FOR SEQ ID NO: 41:

SEQUENCE CHARACTERISTICS:
LENGTH: 55 base pairs

TYPE: nucleic acid

""PANDEDNESS: single
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                                                                                                                         APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John
APPLICANT: McCoy, John
APPLICANT: Mexister, Edward
APPLICANT: Recie, Lisa
APPLICANT: Treacy, Maurice
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Viki
TITLE OF INVENTION: EXCRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: Massachusetts
Conners Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 0.1%; Score 37; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 37; Conservative 0; Mismatches
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATECHIIN BALEASE #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/113,646A
FILING DATE: 31-AUG-1993
FRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/07/084,406
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatibl
OPERATING SYSTEM: PC-DOS/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: SI
TOPOLOGY: linear
MOLECULE TYPE: RNA
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CITY: ARLINGTON
STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
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1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNA (genomic)
  compatible
PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 55;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMMBER: US/08/702,344
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELEPHONE: (617) 498-8224
TELEPHONE: (617) 498-8224
TELEPHONE: (617) 498-8224
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 Dase pairs
TYPE: nucleic acid
official control of the cont
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
US-08-702-344-22/c
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NAME: BIOWN, SCOTT A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 69 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TORNICY: 11002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 0.1%; Score 37; DB 2; Length 69; Best Local Similarity 100.0%; Pred. No. 0.0014; Matches 37; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 5723315
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 22,
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APPLICANT: McCoy, John
APPLICANT: LaVallie, Edward
APPLICANT: Racle, Lisa
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CAPPLICATION DATA: PAPLICATION NUMBER: US/08/702,344 FILING DATE: CLASSIFICATION: 536
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
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; MOLECULE TYPE: cDNA
US-08-702-344-22
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Search completed: March 30, 2000, 00:47:59
Job time: 75541 sec

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Page 8

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Title:
Perfect score:
Sequence:
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Maximum DB seq length: 105
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30001
1 GTGTCACTCACGTTCAGCTA.....AACAACAGTTGCAGAATTGA 30001
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Copyright (c) 1993 - 2000 Compugen Ltd
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44: gb_est25: *
46: gb_est26: *
46: gb_est26: *
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48: gb_est26: *
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53: em_est22: *
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56: gb_est22: *
56: gb_est22: *
66: gb_est23: *
66: gb_est33: *
66: gb_est33: *
67: em_est22: *
68: em_est22: *
67: em_est23: *
68: em_est28: *
69: gb_est44: *
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72: gb_est44: *
73: gb_est44: *
74: gb_est44: *
75: em_est23: *
76: em_est23: *
77: em_gss11: *
77: em_gss3: *
77: em_est23: *
77: em_gss3: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ი	Result No.
٢	10 H
58	ult Query No. Score Match Length DB ID
0.2	% Query Match
65	Length
18	BB
c 1 58 0.2 65 81 B36140 B36140 HS-1038-A1	ID
B36140 HS-1038-A1-	Description

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RESULT 1
B36140/c
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                    ACCESSION
VERSION
KEYWORDS
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AUTHORS
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                                                                                                                                                                  TITLE
Tagged Connectors
Unpublished (1997)
Contact: Mahairas GG, Zackrone KD,
University of Washington
Seattle, WA 98195
Tel: (206) 616-8744
                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 65)
1 (bases 1 to 65)
Mahairas,G.G., Zackrone,K.D., Smith,T., Tipton,S., Schmidt,S.,
Mahairas,G.G., Zackrone,K.D., Smith,T., Tipton,S., Schmidt,S.,
Traicoff,R., Abajian,C., Blanchard,A., West,A. and Hood,L.E.
Construction of a Characterized Clone Resource for Genomic
Sequencing: Generation and Preliminary Analysis of 20,000 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                          B36140 65 bp
HS-1038-A1-D06-MR.abi
sapiens genomic clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B36140.1 GI:2535509
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922
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AR603742

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AR0282107

AR028216

AR083168

AR0831
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CIT Human Genomic Sperm Library C Homo
Plate=CT 820 Col=11 Row=G, genomic survey
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N54156 yv63911.s1
H61099 yr53c112.r1
AU072757 AU072757
D20989 HUWGS01971
H67549 yu68f10.s1
R60869 yh08c10.s1
R60869 yh08c10.s
AR44282107 RFC111-94
C25772 C25772 Dict
R401035772 Dict
R40103507 RFC11-94
R40282107 RFC11-94
R401038300 HWFD93609.r
R53R854 HSPD10934 AR42861 R57801.s
R73R8540 GMP1609 SA
R73R8540 HSPD10834 AR
R73R8549814 tab7a01.x
R73R857 TX06f09.s
R73R8562 ZW75h09.s
R73R8767602.s
R73R8767602.s
R73R8767602.s
R73R87767602.s
R73R874144 S23C8767602.s
R73R855145 N107904.s
R1241884 GUS9511.x
R40866155 XC77d05.x
R40086155 XC77d05.x
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AA916300 cn22c08.s
AI914923 tr27c98.x
H61099 yr51c12.r1
AA082205 zn26h12.r
AA082205 zn26h12.r
AU038446 AU038446
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JOURNAL
COMMENT
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
       BASE COUNT
ORIGIN
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AA780764/c
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Best Local S
Matches 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9842 GGTTAATTTTTGTATTTTTAGTAGAGACGGGGTTTCACCATGTTGGTCAGGCTGGTCT 9899
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                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutharia; Primates; Catarrhini; Hominidae; Homo.

Eutharia; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 91)

E 2 (bases 1 to 91)

E 3 (bases 1 to 91)

E 3 (bases 1 to 91)

E 4 (bases 1 to 91)

E 5 (bases 1 to 91)

E 5 (bases 1 to 91)

E 6 (bases 1 to 91)

E 6 (bases 1 to 91)

E 7 (bases 1 to 91)

E 7 (bases 1 to 91)

E 8 (bases 1 to 91)

E 9 (bases 1 to 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eax: (206) 685-7301
Email: Kzackron@u.washington.edu
Sequence Tagged Connector
Plate: CT 820 row: G column: 11
Class: BAC ends
High quality sequence stop: 65.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA780764
ac68f12.
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AA780764
AA780764.1
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 0.2%; score 58;
Similarity 100.0%; Pred. No.
58; Conservative 0; Mismatci
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/clone=1b="Stratagene fetal retina 937202"
/sex="mixed"
/sex="mixed"
/lab_host="SOLR (kanamycin resistant)"
/lab_host="Solr (kanamycin resistan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 81;
. 5.4e-08;
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ACCESSION
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AUTHORS
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AA916300/c
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DEFINITION
                                                                                                                               Query Match
Best Local S
Matches 51
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Best Local Similarity
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                                             source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 92)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Tumor Gene Index
On May 5, 1995 this sequence version replaced gi:797742.

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550

Emmail: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
Contact: Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              on22c08.s1 similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Insert Length: 1519 Std Error: Seq primer: -40ml3 fwd. ET from High quality sequence stop: 61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                               h 0.2%; S
Similarity 100.0%;
51; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ww-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
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llarity 100.0%; P
Conservative 0;
                                                                                                                                                                                                                                                 /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. " a 34 c 21 g 22 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1557422"
/clone_1ib="NCI_CGAP_Lu5"
                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="carcinoid"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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NCI_CGAP_Lu5 Homo
contains Alu repet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GI:3055692
                                                                                                                               b; Score 51; DB
b; Pred. No. 7e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 53;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-JUN-1998 Homo sapiens cDNA clone IMAGE:1557422 3' repetitive element;, mRNA seamence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                  DB 40;
7e-06;
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                                                                                                                                                                     Length 92;
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KEYWORDS
SOURCE
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H61099/c
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AUTHORS
TITLE
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DEFINITION
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AI914923
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VERSION
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Best Local
                           AUTHORS
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                                                                                                                                                                       H61099
H61099.1
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammal Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 95)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,)
                                                                                                                                                    EST
                                                                                                                                                                                                        H61099 95 bp
yr51c12.r1 Soares feta
IMAGE:208822 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
On May 1, 1997 this sequence version
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AI914923 72 bp mRNA EST 28-JUL-1999 tr27e08.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone IMAGE:2219558 3'similar to contains Alu repetitive element; mRNA sequence.
                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: -40UP from Gibco
Location/Qualifiers
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eutheria; Primates; 1 (bases 1 to 72)
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                                                                                                                                                                                                                                                                                                                                                                                                                                        0.2%; Score 47; ilarity 100.0%; Pred. No. Conservative 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.35 kb. Tumor types include: mixed Mullerian tumor, papillary serous, clear cell, spindle cell. All are primary tumors, metastasis positive. Life Technologies catalog #: 11534-013"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
/clone="IMAGE:2219558"
/clone_lib="NCI_CGAP_Ov23"
/tissue_type="tumor, 5 pooled (see description)"
/lab_host="DH10B"
                                                                                                                                                                       GI:1013931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                             bp mRNA
fetal liver spleen
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                                                                                                                                                                                                            sequence
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0.00014;
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1NFLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 72;
                                                                                                                                                                                                                                    Homo sapiens cDNA clone
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                                                                                                                                                                                                                                                         06-OCT-1995
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Marra, M.,

Gaps

COMMENT

FEATURES

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 68)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Mohling,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M.
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On Sep 21 1992 this sequence version replaced g1:279312
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
Insert Size: 1755
High quality sequence stops: 87
Source: IMAGE Consortium, LLNL
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1755
Std Error: 0.00
Seq_primer: M13RP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA082205 68 bp mRNA EST 23-DEC-1997
Zn26h12.rl Stratagene neuroepithelium NTZRAMI 937234 Homo sap:
cDNA clone IMAGE:548615 5', mRNA sequence.
AA082205
AA082205 1 GI:1624264
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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Generation and analysis of 280,000 human expressed sequence tags
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Location/Qualifiers
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//lab_host="DH10B (ampicillin resistant)"
//lab_host="DH10B (ampicillin resistant)"
//note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
//note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
//note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
//note="Draw was primed with a Pac I - oligo(dT) primer
//note="DNA was primed with a Pac I - oligo(dT) primer
//note="DNA was primed with a Pac I adaptors
//note="DNA was ligated to Eco RI adaptors
//note="DNA was ligated to Eco RI
//note="DNA was ligated t
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/clone="IMAGE:208822"
/clone_lib="Soares fetal liver spleen lNFLS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="GDB:3777953"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
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VERSION
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Best Local S
Matches 43
                                                                                                                                                                    TITLE
JOURNAL
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Local Similarity 100.08;
les 43; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA082205
zn26h12.rl (
cDNA clone )
AA082205
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Fax: 314 286 1810
                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.

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1 (lbase 2 to 68)

1 (lbase 3 to 68)

1 (lbase 4 to 68)

1 (lbase 4 to 68)

1 (lbase 5 to 68)

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1 (lbase 6 to 68)

1 (lbase 7 to 68)

1 (lbase 8 to 68)

2 (lbase 8 to 68)

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4 (lbase 8 to 6
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                                                                                                               Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996) 97044478
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Washington University School of Medicine
                                           On Sep 12, 1996 this sequence version replaced Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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/db_xref-"GDB:3927131"
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Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens
IMAGE:548615 5', mRNA sequence.
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; Pred. No. 0.0027;
0; Mismatches 0;
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BASE COUNT

Query Match Best Local

RESULT AA082205

ACCESSION VERSION

DEFINITION

KEYWORDS

ORGANISM

REFERENCE AUTHORS

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LOCUS
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Best Local Similarity
                                                                                                                                                                                                        MEDLINE
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                                     source
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University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
                                                                                                                                                                                                                                                       Morio, T., Urushihara, H., Saito, T., Ugawa, Y., Mizuno, H., Yoshida, M., Yoshino, R., Mitra, B.N., Pi, M., Sato, T., Takemoto, K., Yasukawa, H., Williams, J., Maeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y. The Dictyostelium developmental cDNA project: generation and analysis of expressed sequence tags from the first-finger stage of analysis of expressed sequence tags from the first-finger stage of
                                                                                                                                                                                                                                                                                                                                                                                            Dictyostelium discoideum.
Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AU038446 93 bp mRNA EST 29-MAR-1999
AU038446 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium
discoideum cDNA clone SSH729, mRNA sequence.
AU038446
                                                                                                                                                                                 On Dec 5, 1997 this sequence version replaced g1:2662913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMAGE Consortium (info@image.llnl.gov)
Seq primer: -28M13 rev2 from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WARNING: There is evidence that suggests that the 384-well parent plate of this clone contains both human and mouse derived clones. Thus, the origin of this clone is uncertain. This caution should kept in mind should you use this clone.
                                                                  Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT = 'Dictyostelium discoideum cDNA project in Japan'
                                                                                                                                                                                                                        DNA Res. 5 (6), 335-340 (1998)
                                                                                                                                                                                                                                              development
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Location/Qualifiers
                                                                                                                                                                   Contact: Hideko Urushihara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
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E Consortium (info@image.llnl.gov) for further i
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314 286 1810
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/clone="IMAGE:548615"
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/db_xref="GDB:3927131"
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100.0%; Pred. No.
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1 (bases 1 to 101)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chiasee,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Halman,M., Kucaba,T., Favello,A., Le,N., Le,N., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Chiapelli,S., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Mardis,E., Moore,B., Morris,M., Bonald, Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R., and Marra,M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N54156 101 bp mRNA EST 28-JAN-1997 yv63gll.sl Soares fetal liver spleen lNFLS Homo sapiens cDNA clone IMAGE:247460 3' similar to contains element MER1 repetitive element
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Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On Nov 22, 1995 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807\text{-}828 (1996) 97044478
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                  48
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/dev_stage="20 week-post conception fetus"
//dev_stage="20 week-post conception fetus"
//lab_host="DH10B (ampicillin resistant)"
//note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
//note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
//note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
//note="Organ: Side_1: Pac I; Side_2: Eco RI;
//note="Organ: Side_1: Pac I; Side_2: Eco RI;
//note="Organ: Side_1: Pac I; Side_2: Eco RI;
//note="Organ: Side_1: Pac I; Side_1: Pac I;
//note="Organ: Side_1: Pac I; Side_2: Pac I; Side_2: Pac I;
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//note="Organ: Side_1: Pac I; Side_2: P
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/db_xref="GDB:3796706"
/db_xref="taxon:9606"
/clone="IMAGE:247460"
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; Pred. No. 0.0022;
0; Mismatches 0
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RESULT 1
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On Nov 22, 1995 this sequence version replaced gi:1070798.
Contact: Wilson RK
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Tex: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hillier, L., Lennon G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chiasoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Le, M., Le, M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 636 Std Error: 0.00
Seq.primer: ml3 -40 forward
High quality sequence stop: 89.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 101)
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N54156.1 GI:1195322
   Similarity
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                                                                                                                                                                           48
                                                                                                                                                           /db_xref="taxon:9606"
/clone="IMAGE:247460"
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/db_xref="GDB:3796706"
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   0.1%;
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   Score 43;
Pred. No.
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DB 25;
0.0021;
                                       Length 101;
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On Sep 21, 1992 this sequence version replaced g1:279312.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarriini; Hominidae; Homo.

1 (bases 1 to 95)

Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., London, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Tangaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
Insert 51ze: 1755
High quality sequence stops: 87
High quality sequence stops: 187
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
INSERT Length: 1755 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 87.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Insert Length: 175
Seq primer: M13RP1
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                                                                                            44
                                                                                     /db_xref="taxon:9606"
/clone="IMAGE:208822"
                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="GDB:3777953"
                                                                                                                                                                                                                                                                                                                           /sex="male"
                                                                                                                                                                                                                                                                                                                                             lone_lib="Soares fetal liver spleen lNFLS"
Score 42;
Pred. No.
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                   DB 24; Length 95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On Jun 5, 1998 this sequence version replaced gi:3188495. Contact: Hideko Urushihara
Institute of Biological Sciences
University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT - Dictyostelium discoideum cDNA project in Japan.
                                                                                                                                                                                   1 (bases 1 to 87)
Okubo,K., Fukushima,A., Yoshii,J., Niiyama,T., Kojima,Y.,
Yoshinari,H., Arimoto,J. and Matsubara,K.
Gene expression of human promyelocytic cell line HL60 before and
after induction of differentiation. A new application of 3'directed
                                                                                                                                                                                                                                                                                                                                                                                               HUMGS01971 Human promyelocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AU072757 73 bp mRNA EST 24-JUN-1999 AU072757 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium discoideum cDNA clone SSA765, mRNA sequence.
                                                                                                      Contact: Okubo,K., Fukushima,A., Yoshii,J., Niiyama,T., Yoshinari,H., Arimoto,J. and Matsubara,K. Institute for Molecular and Cellular Biology
                                                                                                                                                     CDNA sequencing Unpublished (1993)
                                                                                                                                                                                                                                                                                                                                                                                   mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Developmental cDNA in Dictyostelium discoideum (1999)
Onpublished (1999)
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                                                                            va University
Yamada-oka,S
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="mp0383"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Dictyostelium discoideum
/dev_stage="slug"
0 c l g 26 t
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/clone="SSA765"
                                                             Location/Qualifiers
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100.0%; Pred. No.
                                                                            Suita,Osaka 565,Japan
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yu68f10.sl Weizmann Olfactory Epithelium Homo sapiens cDNA clone
IMAGE:238987 3', similar to contains Alu repetitive element;contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Source: IMAGE Consortium, LLNL ;
This clone is available royalty-free through LLNL ;
IMAGE Consortium (info@image.llnl.gov) for further i
Seq primer: Promega -21ml3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On Oct 18, 1995 this sequence version replaced g1:1026289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/dev_stage="01factory epithelium"
/dev_stage="35 year old"
/dev_stage="35 year old"
/lab_host="SOLR cells (kanamycin resistant)"
/lab_host="Solr cells (kanamycin resistant)
/lab_host="lab, kanamycin resistant)
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/clone="IMAGE:238987"
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Matches Query Match Best Local S

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R60869
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The WashU-Merck (1995)

On Apr 18, 1995 this sequence version replaced gi:775532.

Contact: Wilson RK

WashIngton University School of Medicine

4444 Porest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Email: est@watson.wustl.edu

Insert Size: 1405

High quality sequence stops: 76 Source: IMAGE Consortium, Lini This clone is available royalty-free through Lini; contact the IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1405

Std Error: 0.00

Seg primer: SP6

High quality account the common terms. 76
                                                                                                                                      41; Conservative
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1 (bases 1 to 102)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rikkin,L., Rohlfing,T., Soares,M., Tan,F., Tansakis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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yh08c10.s1 Soares infant brain 1NIB Homo
IMAGE:42595 3', mRNA sequence.
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//dev_stage="73 days post_natal"
//lab_host="DH10B (ampicillin resistant)"
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/sex="female"
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Search completed: March 29, 2000, 20:38:58 Job time: 62592 sec

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AR051487 Sequence
D28457 Human mRNA
M87899 Human STS U
AF087511 Homo sapi
L30907 Human STS U
AR051522 Sequence
L36838 Homo sapien
AR051521 Sequence
AR051521 Sequence
L36838 Homo sapien
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L36836 Homo sapien
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L36836 Homo sapien
L39139 Human STS U
AR051525 Sequence
S62605 C1-Inhibito
M36133 Human spien
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M36133 Human low d
M15355 Human low d
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AR051499 Sequence Description

A08911 H.sapiens (M87896 Human carci G32655 A009130 Hum Z50878 H.sapiens (AR051490 Sequence L30829 Human STS U

L36836 Homo sapien

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A08915 H.sapiens (
M36134 Human alpha
M36135 Human alpha
G38859 TA50 Plasmo
X78616 G.gallus ge
L30306 Human STS U
L31225 Human STS U

A08899 H.sapiens (A68621 Sequence 1 AF087511 Homo sapi L29843 Human STS U

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Patent: US 5830670-A 69 03-NOV-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 0.2%;
1 Similarity 100.0%;
58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unclassified.

1 (bases 1 to 76)

1 (bases 1 to 76)

de la Monte, S. and Wands, J.R.

Neural thread protein gene expression and detection of Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                   disease
Patent: US 5830670-A 57 03-NOV-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                      Unclassified.
Unclassified.
1 (bases 1 to 60)
1 (bases, 3, and Wands, 3.R.
de la Monte, S. and Wands, 3.R.
Neural thread protein gene expression and detection of Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 57 from patent
AR051487
AR051487.1 GI:5974851
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                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 48)
                                                                                                                                        HUMHH116 48 bp mRNA PRI 07-FEB-1999 Human mRNA for histone HID, 5'UTR (sequence from the 5'cap to start codon).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unknown
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Direct Submission Submitted (03-FEB-1994) to the DDBJ/EMBL/GenBank databases. Seishi
                                                                               Homo sapiens (library:HT-1080/pKA1) fibrosarcoma CDNA to mRNA, clone HP00474.
                                                                                                       D28457.1 GI:461197
histone HlD.
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                        Kato, S
                                                                                                                                                                                                                                                                                    Similarity
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ilarity 100.0%;
Conservative
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19 c 18 g
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14 c 15 g
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; Pred. No. 2.9e-17;
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US 5830670.
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HUMALCE272/c
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12760 ATGGGGGTTTGCACTGTACCGAAGTTTTGATTCTCAACATGTCC 12807
1 ATGGGGGCTTTGCCACTTGTACCCGAGTTTTTGATTCTCAACATGTCC 48
                                                                                                                                                             Homo sapiens male embryo carcinoma cDNA to other RNA.
Homo sapiens male embryo carcinoma cDNA to other RNA.
Homo sapiens
Eukharyota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 104)
Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.
Alu RNA transcripts in human embryonal carcinoma cells. Model
post-transcriptional selection of master sequences
J. Mol. Biol. (1992) In press
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                                                                                                                                                                                                                                                                                                                                                                                           Alu repeat
                                                                                                                                                                                                                                                                                                                                                                                                                 M87899
M87899.1 GI:174875
                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMALCE272 104 bp ss-RNA PRI Human carcinoma cell-derived Alu RNA transcript,
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48; Conserv
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4-4-1 Nishi-Ohnuma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kato S., Sekine, S., Oh, S.W., Kim, N.S., Umezawa, Y., Yokoyama-Kobayashi, M. and Aoki, T. Construction of a human full-length cDNA bank Gene 150 (2), 243-250 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phone: 0427-42-4791
Fax: 0427-49-7631
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/product=histone HID"
/protein_id="BAA05823.1"
/db_xref="GI:4433162"
/translation="MS"
a 14 c 73
                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="NTera2D1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_line="HT-1080"
/clone_lib="HT-1080/pKA1"
/tissue_type="fibrosarcoma"
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/db_xref="taxon:9606"
/dev_stage="embryo"
/sex="male"
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100.0%; Pred. No. 1.4e-13;
tive 0; Mismatches 0;
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clone CE272.
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/tissue_type="carcinoma"

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RESULT 6
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                                    DEFINITION
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AF087511 66 bp mRNA PRI 13-SEP-1999
Homo sapiens clone ENaC+22 epithelial sodium channel alpha subunit
(SCNNIA) mRNA, alternatively spliced, partial sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STS; PCR primer; STS sequence; microsatellite DNA; microsatellite marker; sequence tagged site; tetranucleotide repeat. Homo sapiens DNA. Homo sapiens DNA. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 5) (bases 1 to 5) (bases 1 to 5) (Berken, S.C., Matsunami, N., Plaetke, R., Albertsen, H., Ballard, L., Melis, R., Lawrence, E., Moore, M., Holik, P.R., Carlson, M., Zhao, X., Robertson, M., Bradley, P., Elsner, T., Tingey, A., Lalouel, J.-M. and
                                                                                                                                                                                                    36;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Cycles Denaturation Annealing Extension (2 10 sec. 56 C 10 sec. 72 C 20 sec. 30 Sec. 56 C 10 sec. 72 C 20 sec. Mg++: 1.00 mM (3 Acrylamide 7%, Formamide 32%, Urea 34%)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e-mail: sts@corona.med.utah.edu
Primer A: CGAGACTCCGTCAAAGAAA
Primer B: CCATTCCAACTTCTTCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genetic and physical mapping of simple sequence repeat containing sequence tagged sites from the human genome Unpublished (1994)
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Human STS UT1543,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted by: Utah Center for Human Genome Research University of Utah, Dept. of Human Genetics
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Similarity 100.0%;
41; Conservative (
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/db_xref="taxon:9606"
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O;
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. 3.1e-07;
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TITLE
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Best Local Similarity
Matches 36; Conserv
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56 C 10 sec.
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Oh,Y. and Warnock,D.G.
Direct Submission
Submitted (26-AUG-1998) Medicine,
Birmingham, AL 35294, USA
                                                                                                  Utah, Dept. of Human Genetics
2160 Eccles Institute of Human Genetics
Salt Lake City, UT 84112
e-mail: sts@corona.med.utah.edu
Primer A: CGAGACTCCGTCAAAGAAA
Primer B: CCATTCCAACTTCTTCCATG
                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 57)

1 (bases 1 to 57)

Gerken, S.C., Matsunami, N., Plaetke, R., Albertsen, H., Ballard, L., Melis, R., Lawrence, E., Moore, M., Holik, P.R., Carlson, M., Zhao, X., Robertson, M., Bradley, P., Elsner, T., Tingey, A., Lalouel, J.-M. and
                                                                                                                                                                                                                                                                                                                                                                                                          L30907.1 GI:624443
STS; PCR primer; STS sequence; microsatellite DNA; microsatellite marker; sequence tagged site; tetranucleotide repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMUT1543A 57
Human STS UT1543,
                                                                                    End to Label: Primer A
                                                                                                                                                                                                                Genetic and physical mapping of simple sequence repeat containing sequence tagged sites from the human genome Unpublished (1994)
                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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Oh, Y. and Warnock, D.G.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                 Initial Denaturation: 94C 300sec
                                                                                                                                                                                                 Submitted by: Utah Center for Human Genome
                                                                                                                                                                                                                                                                  White, R.
                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens DNA.
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<1. .>66
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20 c 2
                 Denaturation
. 56 C 10 se
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/db_xref="taxon:9606"
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72 C 20 sec. Mg++:
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Pred. No. 3.1e-07;
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HUMALUANCC/c
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Homo sapiens 4000 year old remains from Nekht-ankh Alu repeat
fragment 12:4.
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1 (bases 1 to 85)

de la Monte,S. and Wands,J.R.

Neural thread protein gene expression and detection of Alzheimer's
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Sequence 92 from patent US 5830670.
AR051522
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Patent: US 5830670-A 92 03-NOV-1998;
Location/Qualifiers
                                        Ancient DNA: extraction, characterization, molecular cloning, and enzymatic amplification
Proc. Natl. Acad. Sci. U.S.A. 86 (6), 1939-1943 (1989)
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                            89184542
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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27 c 25 g
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/db_xref="taxon:9606"
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A25212/c
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Best Local Similarity 100.0%; Pred. No. 3.6e-06;
Matches 34; Conservative 0; Mismatches 0;
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1 (bases 1 to 35)
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de la Monte,S. and Wands,J.R.
Neural thread protein gene expression and detection of Alzheimer's
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Sequence 91 from patent US 5830670.
AR051521
AR051521.1 GI:5974885
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Location/Qualifiers
1. .84
                                                                                                                                                                                                                                                                                    A25212 35 bp DNA PAT 11-APR-1995
Inter-Alu specific primer DNA (pdj33) from patent WO9213101.
                                                                                                           METHOD OF DETECTING DNA SEQUENCE VARIATION PATENT: WO 9213101-A 3 06-AUG-1992; Location/Qualifiers

1. .35
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/isolate="4000 year old remains from Nekht-ankh"
/db_xref="taxon:9606"
/tissue_type="liver"
<1. .>42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="unknown"
29 c 21 g
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10 c 17 g
                                                          /organism="synthetic construct"
/db_xref="taxon:32630"
10 c 11 g 6 t
 0.1%;
   Score 33;
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08-OCT-1997
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"DETECTING METHOD FOR DNA ARRANGEMENT VARIATION";
Patent number JP 1995115999-A/3, 09-MAY-1995.
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Artificial sequences.
JP 1995115999-A/3
09-MAY-1995
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llarity 100.0%;
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/db_xref="taxon:32644"
/organism="unidentified"
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JOURNAL
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Best Local
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Best Local Similarity
Matches 33; Conserv
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                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                           26168 TTTGGGAGGCCGAGGCGGGCGGATCACGAGGTC 26200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                            repeat_region
                                                                                                                 33 TTTGGGAGGCCGAGGCGGGCGGATCACGAGGTC
HUMUT578A 69 bp DNA
Human STS UT578, 5' primer bind, sequence tagged site.
L39139 L18336
L39139.1 G3:642101
STS; PCR primer; STS sequence; microsatellite DNA; microsatellite marker; sequence tagged site; tetranucleotide repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                          HUMALUANCB 65 bp
Homo sapiens 4000 year
L36836
L36836.1 GI:556194
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Resnick,M.A., Larionov,V.L., Kouprina,N.Y. and Perkins,E.L.
TRANSFORMATION-ASSOCIATED RECOMBINATION CLONING
PAtent: WO 9801573-A 15-JAN-1998;
US HEALTH (US)
                                                                                                                                                                                                                                                                                                                        Ancient DNA: extraction, characterization, molecular cloning, enzymatic amplification proc. Natl. Acad. Sci. U.S.A. 86 (6), 1939-1943 (1989)
                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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unidentified
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ilarity 100.0%;
Conservative
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                                                                                                                                                                                                                                           /organism="Homo sapiens"
/isolate="4000 year old r
/db_xref="taxon:9606"
/tissue_type="liver"
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/db_xref="taxon:32644"
12 c 13 g
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17 c 21 ;
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tive 0; Mismatc
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Nekht-ankh Alu repeat
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REFERENCE
AUTHORS
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ORGANISM
                                                                                                                                                                                                                                              Oy 15491 GTTGGCCAGGCTGGTCTCGAACTCCTGACCTCA 15523
Db 36 GTTGGCCAGGCTGGTCTCGAACTCCTGACCTCA 4
Search completed: March 30, 2000, 07:33:31 Job time: 101360 sec
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ORIGIN
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NAL Unpublished (1994)

Submitted by: Utah Center for Human Genome Research University of Utah, Dept. of Human Genetics

2160 Eccles Institute of Human Genetics

2161 Eccles Institute of Human Genetics

Salt Lake City, UT 84112

e-mail: sts@corona.med.utah.edu

primer A: AGTYCGAGACAGCCTGGC

Primer B: AGGTGGCAGAAAATCGCATC

End to Label: Primer A

PCR Profile:

Initial Denaturation: 94C 300sec

Cycles Denaturation Annealing Extension 5

Cycles Construction Annealing Cycles Denaturation Annealing Cycles Cycles Denaturation Annealing Cycles Cyc
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Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 69)

Gerken, S.C. Matsunami, N., Plaetke, R., Albertsen, H., Ballard, L.,

Melis, R., Lawrence, E., Moore, M., Holik, P.R., Carlson, M., Zhao, X.,

Robertson, M., Bradley, P., Elsner, T., Tingey, A., Lalouel, J.-M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="STS UT578 5' end"
/evidence=experimental
26 a 16 c 14 g 13 t
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/db_xref="taxon:9606"
/map="19"
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Scoring table:

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1 TTATTATGACAAAATTAAAT.....TACAGATACTCTTGCAGTTT 30001
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                                                                         GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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V83635
Q95177
Q33639
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Q71808
Q71814
Q71809
Q71809
Q27391
V19044
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T65729
Q34140
Q33852
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V19044
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Oligonucleotide 1
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Repeat sequence fr
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Repeat sequence fr
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Alu PCR primer 1.
Oligomer LAP322 fo
Alu PCR primer 1.
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Polyester coding s
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Inter-Alu specific
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Inter-Alu s
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                                                                     RESULT
Q71808
ID Q7
AC Q7
DT 30
DE P8
KW S1
KW S1
KW 51
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Best Local S
Matches 41
O71808 standard; .......
Q71808;
Q7180
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27-AUG-1991;
27-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; Page 42; 82pp; English.

Competition experiments using the DNAseI protection assay showed that an oligonucleotide cont; 15 tandem ATT repeats was an effective competitor for binding of the HeLa factor. This oligo was used to prepare an oligonucleotide affinity column for purification of RIP60 from Chinese hamster cells. The protein recognises and binds to an (ATT)n motif in the dhir gene ori. It can also bind to the yeast ARSI domain B. See Q22753 and Q24811.

Sequence 63 BP; 19 A; 5 C; 6 G; 33 T;
                                                                                                                                                                                                                                                                                                                     (UYRO ) ROCKEFELLER UNIV.
(UYVE ) UNIV OF VERMONT.
Heintz N, Heintz NH, Dailey LA, Caddle
WPI; 92-096839/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide containing RIP60 binding motif (ATT)15.
Dihydrofolate reductase; stably bent DNA; RIP60; RIP100; helicase;
DNA footprinting; (ATT)n binding factor; yeast ARS1;
oligonucleotide affinity column; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Replication initiator protein complex - comprises 60 fractions for diagnosis, treatment and prevention of viral infection and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9203479-A.
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US-573570.
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9. .11
/*tag=
/note=
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Q33804
Q33804
Q83951
T65733
Q34025
Q34035
Q34161
Q33645
T66102
Q33687
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Best Local Similarity
Matches 41; Conser
Gruskin EA;

WPI; 94-27324/34.

WPI; 94-27324/34.

New biocompatible medical devices and articles - using a lactic acid-glycolic acid polyester in which monomer units are individually and specifically determined

Example 2; Page 53; 67pp; English.

The sequences given in Q71814-16 represent fragments of the synthetic polyester genes given in Q71801-02. These fragments were used in the production of the full length polyester gene in the plas pMAL-p2. This plasmid was used so that the polyester could be expression an E. coli cell free medium, as pMAL-p2 is recognised by E. coli
                                                                                                                                                                                                                                                                                            01-JUL-1994.
31-DEC-1993; 112716.
31-DEC-1992; US-999520.
(USSU) US SURGICAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAR-1995 (first entry)
30-MAR-1995 (first entry)
Polyester coding sequence for insertion into pMAL-p2.
Synthetic gene; synthesis; polyester; a-amino acid analogue; clips;
stop codon; stop signal; monomer unit; lactate; glycolate; staples;
translation initiation; modified; Met-tRNAf; cyanogen bromide; pins;
co-polymer; sutures; drug delivery device; screws; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         co-polymer; sutures; drug delivery device; screws; ds \mbox{\it Synthetic.}
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CA2112716
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Pred. No.
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                                                    be expressed
E. coli
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                                                                                                 the plasmid
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RESULT
Q71809
             δõ
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DR New biocompatible medical devices and articles - using a lactic relation by 4-273324/34.

Provided the medical devices and articles - using a lactic provided to the provided the medical polyester in which monomer units are individually and specifically determined the provided transcription contains the 5 fragment of the synthetic genes which encode polyesters, contains the 5 fragment of the synthetic genes which encode polyesters, contains the 5 fragment of the synthetic transcription initiator and followed by Poki and Hinddill restriction sites. A further fragment of the synthetic genes were ligated into psport ic to give plasmid psport id (see also Q71810-11), with the final fragment being conserved in a third round of ligation to give psport ie (see also Q71812-13). The E. coli trph initiator sequence was used to express the full length sequences represent synthetic genes which were used in the expressed sequences represent synthetic genes which were used in the correct synthesis of polyesters derived from the a-amino acid analogues of an entire transcription to give a provided to the correct provided
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 41; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         071809 standard; DNA; 103 BP.
071809; (first entry)
30.MAR-1995 (first entry)
30.MAR-1995 (first entry)
spsport-rc synthetic polyester gene 5' fragment and trpA initiator.
synthetic gene; synthesis; polyester; a-amino acid analogue; clips;
stop codon; stop signal; monomer unit; lactate; glycolate; staples;
stop codon; initiation; modified; Met-ERNAf; cyanogen bromide; plns;
translation initiation; and flyery device; screws; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CA2112716-A.
01-JUL-1994.
31-DEC-1993; 112716.
31-DEC-1992; US-999520.
(USSU ) US SURGICAL CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pins and screws.
81 BP; 47 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.1%; Score 41; DB 1; ilarity 100.0%; Pred. No. 0.0036; Conservative 0; Mismatches 0
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19. 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Start codon"
22. 93
/*tag= c
/note= "Polyester gene 5' fragment"
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"trpA initiator
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"Start codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 C;
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RESULT V19044 V19044 V19044 V1904 V1
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Best Local S
Matches 41
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Best Local S
Matches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid except Pro. Of the three stop codons, UAA, UAG and UGA, one of these stop codons is reversed for the stop signal for the polyester. The remaining two stop codons are available for encoding the monomer units of the polyester. Lactate and glycolate are encoded by UAA and UAG, respectively. Initiation of translation always starts at an AUG codon, therefore the first lactate of the chain may be encoded by an AUG codon. This is accomplished through the use of a specially modified Met. tRNAf modified to carry lactate instead of Met. Alternatively, a Met is incorporated in the first position of the polymer chain. The resulting polymer is treated with cyanogen bromide to remove the Met. Co-polymers produced in this manner may be used to produce sutures, staples, clips, drug delivery devices, pins and screws.

Sequence 103 BP; 58 A; 7 C; 9 G; 29 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 6; Page 6; 31pp; English.

Primer PDJ33 is one of several primers which are preferred for use in amplifying inter-Alu regions of DNA. The amplified fragments are then subjected to 2-D electrophoresis on the basis of length and differences in base sequence. The resulting separation pattern is transferred to a filter for screening with a probe. The method can be used to detect genetic variation.

See Q27389-Q27404 and Q33141-Q33144.

Sequence 35 BP; 8 A; 10 C; 11 G; 6 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detection of genetic variation by 2-D electrophoresis of fragments - and hybridisation with labelled probes, carried on fragments consisting of inter-repeat sequences generated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                                                  28-JUL-1998 (first entry)
Alu PCR primer 1.
PCR; primer; amplification; Alu repeat sequence; vector; circular yeast artificial chromosome; YAC; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2146
                                                                                                                                                           V19044 standard; DNA; V19044;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-AUG-1992.
24-JAN-1992; NL0018.
25-JAN-1991; NL-000132.
(INGE-) INGENY BV.
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Polymerase chain reaction; PCR; repetitive element; Synthetic.

W09213101-A.
  Saccharomyces sp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                227391 standard; DNA;
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100.0%; Pred. No. 0.1
Live 0; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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0.0034;
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Best Local S
Matches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    preparation of yeast artificial chromosomes - by in vivo recombination using vector comprising yeast centromere, marker, yeast telomere and nucleic acid for recombination.

Example 1; Page 45; 117pp; English.

This is the nucleotide sequence for the PCR primer used in the amplification of the Alu repeat sequence, which is used to demonstrate the processes described in the invention. It involves the creation and use of circular yeast artificial chromosome (YAC) to selectively clone specific nucleic acids from a background of mixed nucleic acids by introducing the vector(s) into E. coli cells. They can be used to rapidly isolate human DNA where only a part of the sequence of DNA is known. Using the methods large fragments of DNA can be easily cloned and analysed.

Sequence 40 BP; 7 A; 12 C; 13 G; 8 T;
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Q30397 standard; DNA;
Q30397;
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15-JAN-1998.
09-JUL-1996; U11478.
09-JUL-1996; WO-U11478.
(USSH) US DEPT HEALTH & HUMAN SERVICES.
KOUPPINA NY, LATIONOV VL, PERKINS EL, RE
WPI; 98-110234/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human leukocyte adhesion
simplex; AIDS; modified;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1886 TGGCTCACGCCTGTAATCCCAGCACTTTGGGAG
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322 for forming triplex with HUMINTO2 target duplex.
32e adhesion protein; p150,95 alpha subunit gene; he
35; modified; HIV; RSV; HPV; malignancy; hepatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                  /*tag= g
/mod_base=
/note= "OTH
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/mod_base=
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13
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10
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/mod_ba
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/note= "OTHER= N6
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/mod_base=
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Pred. No. 0.7
0; Mismatches
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RESULT
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PI Froehler B, Krawczyk S, Matteucci MD, Milligan J;

DR WP1, 92-217083/26.

PT New Oligomers contg. modified bases - which form a triplex with pr G-C doublet in a DNA duplex, for treating and diagnosing HIV, pr G-C doublet in a DNA duplex, for treating and diagnosing HIV, pr G-C doublet in a DNA duplex, for treating and diagnosing HIV, pr G-C doublet in a DNA duplex, for treating and diagnosing HIV, pr G-C doublet in a DNA duplex, for treating and diagnosing HIV, pr G-C doublet in a G-C duple in the first soligomer is the forman garriang a triplex at protein grower of the duplex. The specific trarget sequence of this oligomer is the human leukocyte adhesion protein p150, 95 and the solumit gene (HUMINFU2) beginning at nucleotide 2370 contg. a grapha subunit gene (HUMINFU2) beginning at nucleotide 2370 contg. a grapha subunit gene (HUMINFU2) beginning at nucleotide 2370 contg. a comparison of the duplex. The oligomer, of the duplex trargets, e.g. HPV, HER; HIV chapter rich sequence concd. on one strand of the duplex. The oligomer, of the chapter is the duplex triple conditions of the sasquers and inflammation. The triple conditions thus assays may be carried out without subjecting the test specimen to harsh conditions. The chapter is conditions of the condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-JUN-1992
25-NOV-1991; U08811.
23-NOV-1999; US-641907.
18-JAN-1991; US-64382.
08-APR-1991; US-683420.
17-APR-1991; US-680544.
17-APR-1991; US-680547.
17-APR-1991; US-680547.
17-APR-1991; US-680546.
27-SEP-1991; US-760733.
15-JAN 1998.
15-JAN 1998.
09-JUL-1996; U11478.
09-JUL-1996; WO-U11478.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
KOUDTINA NY, LATIONOV VL, PETKINS EL, RESNICK MA;
WPI; 98-110234/10.
Preparation of yeast artificial chromosomes - by in vivo recombination using vector comprising yeast centromere, m
                                                                                                                                                                                                                                                                                                   Synthetic.
Saccharomyces sp.
WO9801573-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2158 AATAATAATAATAATAATAATAATAAA 2187
                                                                                                                                                                                                                                                                                                                                                                                                                Alu PCR primer 1.
PCR: primer; amplification; Alu repeat sequence; vector; circular yeast artificial chromosome; YAC; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               modified_base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   V19044 standard; DNA; 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 AATAATAATAATAATAATAATAATAAA 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.1%; Son character 0.1%; Son conservative 0;
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/note= "OTHER= N6 methyl-8-oxo 2' deoxyadenine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
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"OTHER= N6 methyl-8-oxo 2' deoxyadenine'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВÞ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                score 30; DB; Pred. No. 5.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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42

Query Match
Best Local Similarity
Matches 30; Conserv

0.1%; Silarity 100.0%; If Conservative 0;

Score 30; DB; Pred. No. 4.4
0; Mismatches

DB 1; 4.4;

Length 91;

Indels

0

0

2460 AGTCTTGCTCTGTTGCCCAGGCTGGAGTGC 2489

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CC alim 1; Page 2078; 2245pp; Japanese.

CC A single-stranded DNA (or its complementary strand or the corresp.

CC A single-stranded DNA) which comprises one of the 7837 "GS" sequences

CC double-stranded DNA) which comprises one of the 7837 "GS" sequences

CC given in T19001-T26837 and which is able to hybridise to part of

CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)

CC sequences were obtained from 3'-directed CDNA libraries prepared

CC income various human tissues; synthesis of cDNA was initiated from the

CC untranslated sequence is unique to a particular mRNA species, almost

CC untranslated sequence is unique to a particular mRNA species, almost

CC all the 3'-oriented cDNA hybridise with specific mRNAs. Each library

CC is constructed so as to reflect accurately the relative abundance of

CC different mRNAs in the particular tissue from which it was derived.

CC The appearance frequency of a given GS in a cDNA library can be

CC determined (esp. using primers and probes derived from the GS

Sequences) as a means of diagnosing abnormal cell function or for

CC recognising different cell types.

SO Sequence 91 BP; 38 A; 22 C; 11 G; 17 T;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              yeast telomere and nucleic acid for recombination
Example 1; Page 45; 117pp; English.

This is the nuclectide sequence for the PCR primer used in the
amplification of the Alu repeat sequence, which is used to
demonstrate the processes described in the invention. It involves
the creation and use of circular yeast artificial chromosome (YAC)
to selectively clone specific nucleic acids from a background of
mixed nucleic acids by introducing the vector(s) into E. coli cells.

They can be used to rapidly isolate human DNA where only a part of the
sequence of DNA is known. Using the methods large fragments of DNA can
be easily cloned and analysed.

Sequence 40 BP; 7 7 A; 12 C; 13 G; 8 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T26410;
06-DEC-1996 (first entry)
06-DEC-1996 (first entry)
Human gene signature HUMGSO8651.
Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-blased library; diagnosis; detection; cell typing; abnormal cell function; ss.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Matsubara K, Okubo K;
WPI; 95-206931/27.
Identifying gene signatures in 3'-directed human cDNA library -
for diagnosis of abnormal cell function, by preparing cDNA that
reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MATS/) MATSUBARA K. (OKUB/) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T26410 standard; cDNA to mRNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30 AAAGTGCTGGGATTACAGGCGTGAGCCACC 1
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100.0%; Pred. No. 5.
tive 0; Mismatches
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V83640/

ID 3640/

ID 3640
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              Pr Assay for testing the carcinogenic properties of a test substance by introduction of a reporter gene expression vector containing a propertitive DNA sequence that is unstable in cancer cells repetitive DNA sequence that is unstable in cancer cells bisclosure; Page 15; 103pp; English.

CC The present sequence represents an oligonucleotide used in the course of the construction of assay plasmids, which are used in the course of the construction of assay plasmids, which are used in the course of the construction. The specification describes an assay for testing the construction of assay plasmids, which are expression vector comprises introducing into cells a reporter gene expression vector comprising a crepetitive DNA sequence which exhibits instability in cancer cells, conference of the reporter gene, exposing the resulting cells to the test substance and determining whether the test substance is carcinogenic or anti-carcinogenic by comparing the frequency of reporter gene expression in cells which have not been exposed to the test substance. The assay can be used to identify human dietary components that protect against DNA contents of the construction of the construction of the construction cells with the frequency of reporter gene expression in the used to identify human dietary components that protect against DNA constructions.
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Best Local
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W09213101-A.

06-AUG-1992.
24-JAN-1992; NL0018.
25-JAN-1991; NL-000132.
(INGE) INGENY BV.
Uitterlinden AG, Vijg J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q27391 standard; DNA;
Q27391;
27-JAN-1993 (first e
Inter-Alu specific pr
in the result cells which h be used to id instability,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repetitive sequence; ca
DNA instability; cancer
Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in amplifying inter-Alu regions of DNA. The amplified fragments then subjected to 2-D electrophoresis on the basis of length and differences in base sequence. The resulting separation pattern i transferred to a filter for screening with a probe. The method consent to detect genetic variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-OCT-1998.

08-APR-1998; G00869.

08-APR-1997; GB-007141.

(FOOD-) FOOD RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic. W09845476-A1.
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Oligonucleotide 1 used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8859 AAAGTGCTGGGATTACAGGCGTGAGCCA 8886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              be used to detect genetic variation.
See Q27389-Q27404 and Q33141-Q33144.
Sequence 35 BP; 8 A; 10 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detection of genetic variation by 2-D electrophoresis of fragments - and hybridisation with labelled probes, carried on fragments consisting of inter-repeat sequences generated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schweizer M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 6; Page 6; 31pp; English.
Primer PDJ33 is one of several primers which are
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  therefore some
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer; diet;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          reaction;
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Paction; PCR;
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  carcinogenic; human dietary component;
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  types
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  of.
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  cancer, and
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  can
  be used
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PT Assay for testing the carcinogenic properties.

PT by introduction of a reporter gene expression vector containing a propertitive DNA sequence that is unstable in cancer cells Disclosure; Page 16; 103pp; English.

CC The present sequence represents an oligonuclectide used in the course of the construction of assay plasmids, which are used in the course of the construction. The specification describes an assay for testing the carcinogenic properties of a test substance. The assay comprises controducing into cells a reporter gene expression vector comprising a repetitive DNA sequence which exhibits instability in cancer cells, whereby instability of the repetitive DNA sequence affects expression of the reporter gene, exposing the resulting cells to the test substance and determining whether the test substance is carcinogenic or anti-carcinogenic by comparing the frequency of reporter gene expression in the resulting cells with the frequency of reporter gene expression for the used to identify human dietary components that protect against DNA instability, and therefore some types of cancer, and can be used to sequence 46 BP; 2 A; 6 C; 20 G; 18 T;
  RESULT
V83635
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V83641
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Matches 28
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-OCT-1998;
08-APR-1998;
08-APR-1997;
                                                                                                                V83635;
15-OCT-1998.
08-APR-1998; G00869.
08-APR-1997; GB-007141
                                                           Oligonucleotide 1 used in the construction Repetitive oligonucleotide; carcinogenic; Pona instability; cancer; diet; ss.
                                                                                     01-MAR-1999 (first entry)
Oligonuclectide 1 used in
                                    WO9845476-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 99-024011/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide 2 used in the construction of assay plasmids. Repetitive sequence; carcinogenic; human dietary component;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contribute
Sequence
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DNA instability; can
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V83641;
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18 A;
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human dietary component;
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                                                                                                                                                         Query Match
Best Local Similarity
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Best Local Similarity
Matches 28; Conserv
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095177 is a simple tandem repeat (STR) corresponding to the 2nd part of wgla2. The STR can be used for treatment and diagnosts in human and veterinary medicine, partic. for genetic characterisation, mapping, linkage studies and analysis/diagnosis of acquired disease alleles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-DEC-1994; G02789.
21-DEC-1995; GB-026052.
21-DEC-1995; GB-026052.
(UYLE-) UNIV LEICESTER.
Armour J. Jeffreys AJ;
WPI; 95-240682/31.
Identifying simple tandem repeat loci in DNA - by screening DNA
Identifying simple tandem repeats before cloning
and rescreening, also simple tandem repeats for treatment or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O95177; standard; DNA; 57 BP.

O95177; first entry)

O8-FEB-1996 (first entry)

Simple tandem repeat (STR) corresponding to the 2nd part of wgla2.

Simple tandem repeat; STR; wgla2; treatment; genetic; diagnosis;

characterisation; mapping; linkage studies; analysis; alleles;
                                                             2467 CTCTGTTGCCCAGGCTGGAGTGCAGTGG 2494
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WO9517522-A2.
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CTCTGTTGCCCAGGCTGGAGTGCAGTGG 50
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                                                                                                                                                                                                                                                                                           7 A;
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Pred. No.
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RESULT 15
Q33639
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Query Match 0.1%; Score 28; DB Best Local Similarity 100.0%; Pred. No. 17; Matches 28; Conservative 0; Mismatches
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033639;
02-FEB-1993 (first entry)
Microsatellite sequence from clone MTGT13A.
PCR; selection; primers; OPTIPRIM; breeding; cat
genetic mapping; traits; amplification; ss.
Bos taurus.
Bos taurus.
W09213102-A.
06-AUG-1992;
15-JAN-1991; US-642342.
                                                                                                                                                             traits esp. in cattle, to See also Q33501-34437. Sequence 64 BP; 1 A;
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                                    DB 1;
17;
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Search completed: March 30, 2000, 10:53:10 Job time: 111788 sec

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Qy 18619 TGTGTGTGTGTGTGTGTGTGTGCA 18646

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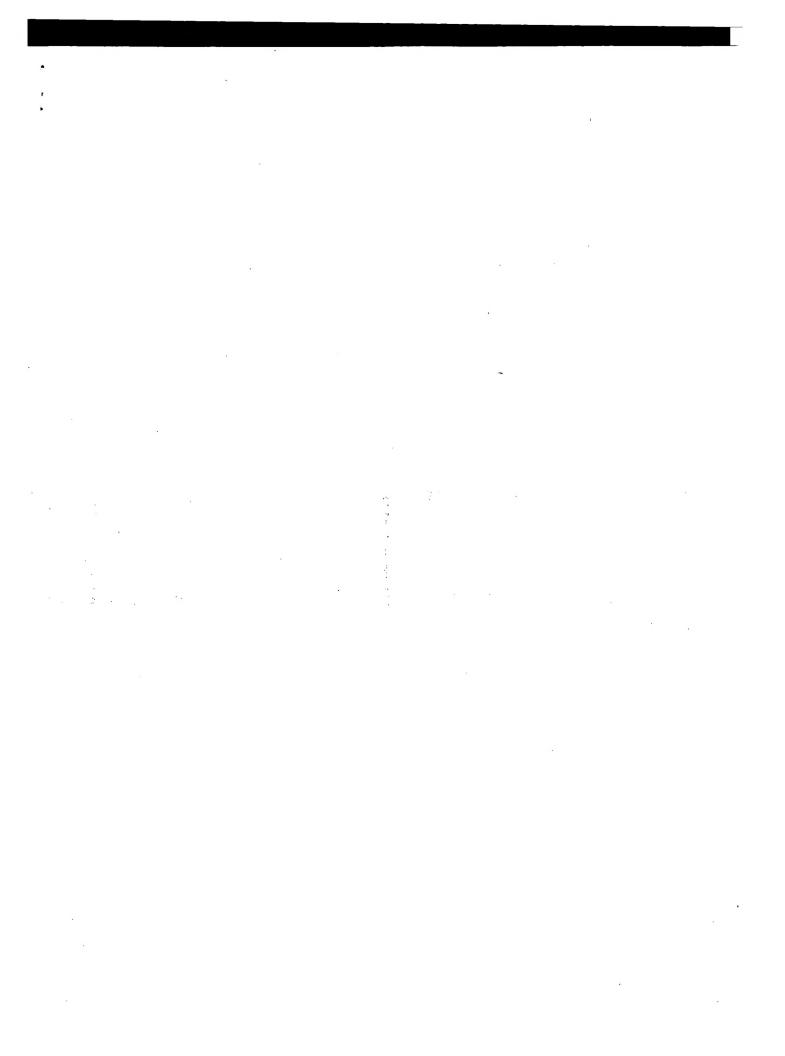
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            GenCore version 4.5 Copyright (c) 1993 - 2000 Com
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US-08-455-627-23	US-08-859-998-66	US-08-859-998-66	PCT-US95-17111A-91	US-08-450-673C-91	US-08-340-426D-91	US-08-454-557C-91	US-08-222-177A-427	US-08-222-177A-131	US-08-222-177A-421	US-08-222-177A-116	US-08-222-177A-424	US-08-222-177A-89	US-08-222-177A-328	US-08-222-177A-346	US-08-222-177A-77	PCT-US95-17111A-67	US-08-450-673C-67	US-08-340-426D-67
Sequence 23, App	Sequence 66, App	•	•	Sequence 91, App	Sequence 91, App	Sequence 91, App									•	•	•	•
	26 0.1 27 1 US-08-455-627-23 Sequence 23,	26 0.1 26 4 US-08-859-998-66 Sequence 66, 26 0.1 27 1 US-08-455-627-23 Sequence 23,	26 0.1 26 4 US-08-859-998-66 Sequence 66, 26 0.1 26 4 US-08-859-998-66 Sequence 65 Sequence 23, 26 0.1 27 1 US-08-455-627-23 Sequence 23,	42 27 0.1 84 6 PCT-US95-17111A-91 Sequence 91, 43 26 0.1 26 4 US-08-859-998-66 Sequence 66, 44 26 0.1 26 4 US-08-859-998-66 Sequence 66, 45 26 0.1 27 1 US-08-455-627-23 Sequence 23,	41 27 0.1 84 d US-08-450-673C-91 Sequence 91, 42 27 0.1 84 6 PCT-US95-17111A-91 Sequence 91, 43 26 0.1 26 d US-08-859-998-66 Sequence 66, 44 26 0.1 26 d US-08-859-998-66 Sequence 66, 45 26 0.1 27 1 US-08-455-627-23 Sequence 23,	40 27 0.1 84 US-08-340-425D-91 Sequence 91, 41 27 0.1 84 GPCT-US95-17111A-91 Sequence 91, 42 27 0.1 84 GPCT-US95-17111A-91 Sequence 91, 43 26 0.1 26 US-08-859-998-66 Sequence 66, 44 26 0.1 26 US-08-859-998-66 Sequence 66, 45 26 0.1 27 1 US-08-455-627-23 Sequence 23,	39 27 0.1 84 US-08-454-557C-91 Sequence 91, 40 27 0.1 84 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1 US-08-455-627-23 Sequence 23,	36 27 0.1 65 US-08-222-177A-421 Sequence 421. 37 27 0.1 72 1 US-08-222-177A-121 Sequence 131. 38 27 0.1 72 1 US-08-222-177A-427 Sequence 217. 39 27 0.1 84 3 US-08-454-557C-91 Sequence 91. 40 27 0.1 84 4 US-08-340-426D-91 Sequence 91. 41 27 0.1 84 4 US-08-450-673C-91 Sequence 91. 42 27 0.1 84 6 PCT-US95-17111A-91 Sequence 91. 43 26 0.1 26 4 US-08-859-998-66 Sequence 66. 44 26 0.1 27 1 US-08-859-998-65 Sequence 66. 45 26 0.1 27 1 US-08-455-627-23 Sequence 23,	35 27 0.1 65 1 US-08-222-177A-116 Sequence 116. 36 27 0.1 65 1 US-08-222-177A-121 Sequence 421. 37 27 0.1 72 1 US-08-222-177A-131 Sequence 131. 38 27 0.1 72 1 US-08-222-177A-427 Sequence 131. 39 27 0.1 72 1 US-08-222-177A-427 Sequence 91. 40 27 0.1 84 US-08-454-557C-91 Sequence 91. 41 27 0.1 84 US-08-450-673C-91 Sequence 91. 42 27 0.1 84 US-08-450-673C-91 Sequence 91. 43 26 0.1 26 US-08-859-988-66 Sequence 66. 44 26 0.1 27 1 US-08-859-988-66 Sequence 66. 45 26 0.1 27 1 US-08-455-627-23 Sequence 23,	34 27 0.1 51 US-08-222-177A-424 Sequence 424. 35 27 0.1 65 1 US-08-222-177A-421 Sequence 116. 36 27 0.1 65 1 US-08-222-177A-421 Sequence 421. 37 27 0.1 65 1 US-08-222-177A-421 Sequence 621. 38 27 0.1 72 1 US-08-222-177A-131 Sequence 131. 38 27 0.1 72 1 US-08-222-177A-131 Sequence 61. 39 27 0.1 84 US-08-454-557C-91 Sequence 91. 40 27 0.1 84 US-08-340-425D-91 Sequence 91. 41 27 0.1 84 US-08-340-425D-91 Sequence 91. 42 27 0.1 84 US-08-859-988-66 Sequence 91. 43 26 0.1 26 US-08-859-988-66 Sequence 66. 44 26 0.1 27 US-08-859-988-65 Sequence 66. 45 26 0.1 27 US-08-455-627-23 Sequence 23,	33 27 0.1 51 US-08-222-177A-89 Sequence 89, 34 27 0.1 51 US-08-222-177A-18 Sequence 424, 35 27 0.1 65 US-08-222-177A-116 Sequence 116, 36 27 0.1 65 US-08-222-177A-12 Sequence 117A-12 Sequence 116, 37 27 0.1 72 US-08-222-177A-131 Sequence 131, 38 27 0.1 72 US-08-222-177A-131 Sequence 131, 38 27 0.1 72 US-08-222-177A-131 Sequence 131, 39 27 0.1 84 US-08-454-557C-91 Sequence 91, 40 27 0.1 84 US-08-459-591 Sequence 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1 US-08-222-177A-424 Sequence 424, 35 27 0.1 65 1 US-08-222-177A-421 Sequence 116, 36 27 0.1 65 1 US-08-222-177A-421 Sequence 121, 37 27 0.1 72 1 US-08-222-177A-421 Sequence 131, 37 27 0.1 72 1 US-08-222-177A-421 Sequence 91, 38 27 0.1 72 1 US-08-222-177A-421 Sequence 91, 38 27 0.1 84 4 US-08-454-557C-91 Sequence 91, 40 27 0.1 84 4 US-08-454-557C-91 Sequence 91, 41 27 0.1 84 4 US-08-459-65 Sequence 91, 42 27 0.1 84 6 PCT-US95-17111A-91 Sequence 91, 42 26 0.1 26 4 US-08-859-998-66 Sequence 66, 45 0.1 27 1 US-08-859-998-66 Sequence 66, 45 0.1 27 1 US-08-455-627-23 Sequence 23, 45 0.1 27 1 US-08-455-627-23 Sequence 23,	29 28 0.1 66 PCT-US95-1711A-67 Sequence 67, 30 27 0.1 35 1 US-08-222-177A-77 Sequence 77, 31 27 0.1 46 1 US-08-222-177A-346 Sequence 346, 32 27 0.1 50 1 US-08-222-177A-328 Sequence 328, 33 27 0.1 51 I US-08-222-177A-89 Sequence 89, 34 27 0.1 51 I US-08-222-177A-16 Sequence 89, 35 27 0.1 65 1 US-08-222-177A-116 Sequence 424, 35 27 0.1 65 I US-08-222-177A-124 Sequence 116, 36 27 0.1 72 I US-08-222-177A-124 Sequence 421, 37 0.1 72 I US-08-222-177A-127 Sequence 421, 38 27 0.1 72 I US-08-222-177A-127 Sequence 421, 38 27 0.1 84 US-08-454-557C-91 Sequence 91, 40 27 0.1 84 US-08-454-557C-91 Sequence 91, 41 27 0.1 84 US-08-450-673C-91 Sequence 91, 42 27 0.1 84 US-08-450-673C-91 Sequence 91, 42 27 0.1 84 US-08-859-998-66 Sequence 66, 45 0.1 26 US-08-859-998-66 Sequence 66, 45 0.1 27 US-08-859-998-66 Sequence 63, 56 0.1 27 US-08-455-627-23 Sequence 23, 56 0.1 27 US-08-455-627-23	28 0.1 66 4 US-08-450-673C-67 Sequence 28 0.1 66 6 PCT-US95-17111A-67 Sequence 27 0.1 35 1 US-08-22-177A-77 Sequence 27 0.1 35 1 US-08-22-177A-77 Sequence 27 0.1 50 1 US-08-22-177A-346 Sequence 27 0.1 51 US-08-22-177A-89 Sequence 27 0.1 51 US-08-22-177A-89 Sequence 27 0.1 51 US-08-22-177A-116 Sequence 27 0.1 65 1 US-08-22-177A-116 Sequence 27 0.1 65 1 US-08-22-177A-131 Sequence 27 0.1 72 1 US-08-22-177A-131 Sequence 27 0.1 72 1 US-08-22-177A-131 Sequence 27 0.1 84 4 US-08-345-651 Sequence 27 0.1 84 4 US-08-345-651 Sequence 28 0.1 26 4 US-08-859-998-66 Sequence 26 0.1 26 4 US-08-859-998-66 Sequence 26 0.1 27 1 US-08-859-998-66 Sequence 27 0.1 84 GUS-08-859-998-66 Sequence 28 Sequence 29 Sequenc

ALIGNMENTS

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RESULT 1
US-08-454-557C-69
US-08-454-557C-69
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NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEPAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 69, Application US/08454557C Patent No. 5830670 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/454,557C

FILING DATE: 30-MAY-1995

CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                    TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1100 New CITY: Washington STATE: D.C.
                                                                                     LENGTH:
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                                                                                        76 base pairs
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Match 0.2%; Score 58; DB 3; Local Similarity 100.0%; Pred. No. 2.5e-10;

Length 76; Indels

Conservative

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Mismatches

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Gaps 27742

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RESULT 3
US-08-450-673C-69
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2640
TELEPHONE: (202) 371-2640
TELEPHONE: (202) 371-2640
                                                                                                                                                             Jatent No. 5948800
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
TITLE OF SPOUENCES: 121
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Ouery Match
Ouery Match
Best Local Similarity 100.0%; Pred. No. 2.5e-10;
Matches 58; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27685 GCCCCGCTAATTTTTGTATTTTTAGTAGAGACAGGGTTTCACCGTGTTGGCCAGGATG 27742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202) 371-254
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 76 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/340,426D
FILING DATE: 14-NOV-1994
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
                                                                                                       STREET: 1100 New ICITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid STRANDEDNESS: both TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 GCCCCGCTAATTTTTGTATTTTTAGTAGAGAGAGGGTTTCACCGTGTTGGCCAGGATG 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Sterne, Kessler, Goldstein & Fox P.L.L.C
1100 New York Avenue, Suite 600
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NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-5600
TELEFAX: (202) 371-2540
NOTELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 76 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
US-08-450-673C-69
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PCT-US95-17111A-69
                                    INFORMATION FOR SEQ ID NO: 65
SEQUENCE CHARACTERISTICS:
LENGTH: 76 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: both
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Ouery Match
Duest Local Similarity 100.0%; Bred. No. 2.5e-10
Matches 58; Conservative O; Mismatches O.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 30-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                              NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340,426
FILING DATE: 14-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Neural Thread Protein Gene Expression TITLE OF INVENTION: Detection of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: de la Monte,
APPLICANT: Wands, Jack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/0 FILING DATE: 30-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1100 New
CITY: Washington
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ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 GCCCCGCTAATTTTTGTATTTTTAGTAGAGACAGGGTTTCACCGTGTTGGCCAGGATG 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D.C.
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Sequence 57, Application ....
Sequence 57, Application ....
Sequence 57, Application ....
Patent No. 5948634

GENERAL INFORMATION:
GENERAL INFORMATION: Medical Suzanne
APPLICANT: Wands, Jack R.
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
TITLE OF INVENTION: of Alzheimer's Disease
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US-08-454-557C-57
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                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-454-557C-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: LUGW19, Steven R.
REGISTRATION NUMBER: 06.09
REFERENCE/DOCKET NUMBER: 06.09
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                 Best
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APPLICANT: de la 1
APPLICANT: Wands,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27685 GCCCCGCTAATTTTTGTATTTTAGTAGAGACAGGGTTTTCACCGTGTTGGCCAGGATG
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CURRENT APPLICATION DATA:
APPLICATION UNBER: US/08/454,557C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
ATTOLUTY TOTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease NUMBER OF SEQUENCES: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid STRANDEDNESS: both TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
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                                                                                                                                                                                                                                                                                                                                                Local
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                                                                                                                                                                                                                                                                                                                             l Similarity 100.
55; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 base pairs
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Wands, Jack R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                              Score 55;
Pred. No.
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40. 2.4e-09;
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 57, Application US/08450673C Patent No. 5948888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION UDUBER: US/08/340,426D
FILING DATE: 14-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,673C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: LUGWIG, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (202) 371-25
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27685 GCCCCGCTAATTTTTGTATTTTTAGTAGAGACAGGGTTTCACCGTGTTGGCCAGG 27739
                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Neural Thread Protein Gene Expression TITLE OF INVENTION: of Alzheimer's Disease NUMBER OF SEQUENCES: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
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STREET: 1100 New Y
CITY: Washington
                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                         CITY: Washington
                                                                                                                                                                                                                                                                                                                                             STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Ludwig, Steven R. REGISTRATION NUMBER: 36,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity es 55; Conserv
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                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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1100 New York Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Sterne, Kessler, Goldstein & Fox P.L.L.C. 1100 New York Avenue, Suite 600
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(202) 371-2540
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0609.3840002
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e, Suite 600
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 base pairs
TYPE: nucleic acid
STRANDEDNESS: both

57

TOPOLOGY:

both

Ouery Match 0.2%; Score 55; DB 4; Le Ouery Match 10.0%; Pred. No. 2.4e-09; Matches 55; Conservative 0; Mismatches 0;

Length 60;

Indels

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Gaps

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RESULT 9
US-08-454-557C-92/c
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; Sequence 57, Application PC/TUS9517111A
; GENERAL INFORMATION:
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                                                                                                                                                                    Query Match
Best Local S
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CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 2005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC COMPUTER: PATENTING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PATENTIN DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                     TELEFAX: (202) 371-254
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 base pairs
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STRANDEDNESS: both
TOPOLOGY: both
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 066
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340,426
FILING DATE: 14-NOV-1994
ATTORNEY/AGRET INFORMATION:
NAME: Ludwig, Steven R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Neural Thread Protein Gene Expression and TITLE OF INVENTION: Detection of Alzheimer's Disease NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/US95/17111A
                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE:
                                                                                                                                                h 0.2%; Score 55; DB 6; I
Similarity 100.0%; Pred. No. 2.4e-09;
55; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Sterne, Kessler, Goldstein & Fox P.L.L.C
1100 New York Avenue, Suite 600
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Wands, Jack R.
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                                                                                                                                                                                        Length 60;
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TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 92

SEQUIENCE CHARACTERISTICS:
LENGTH: 85 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
US-08-454-557C-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 10
US-08-340-426D-92/c
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CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/454,557C
EILING DATE: 30-MAY-1995
CIASGIFTINATION. S1A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 92, Application US/08340426D Patent No. 5948634
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Best Local Similarity
Matches 35; Conserv
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APPLICANT: de la Monte, S
APPLICANT: Wands, Jack R.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/340,426D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840003
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                          APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
                                                                                                                                                                                                                ADDRESSEE: Sterne,
STREET: 1100 New 1
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48 CGGGCGGATCACGAGGTCAGGAGATCGAGACCATC 14
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1100 New York Avenue,
                                                                                                                                                                                                                                                                     E: Sterne, Kessler, Goldstein & Fox P.L.L.C 1100 New York Avenue, Suite 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.1%; Score 35; DB 3; Length 85; 100.0%; Pred. No. 0.0071; ative 0; Mismatches 0; Indels
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FILING DATE: 14 CLASSIFICATION:

14-NOV-1994

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                                                                                 TOPOLOGY:
US-08-450-673C-92
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 Query Match
Best Local Sim
Matches 35;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: D.C.
COUNTRY: U.S.A.
COUNTRY: U.S.A.
ZIP: 20005-9934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                               TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
ADDRESSEE: Store
                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: LUGWIG, SLEWER R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 85 base pairs
                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/450,673C FILING DATE: 30-MAY-1995 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48
                                                                                                            TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
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                  Similarity
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pedness: both
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   Conservative
                                                                                                  both
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0.1%; Score 35; DB
100.0%; Pred. No. 0.0
tive 0; Mismatches
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Pred. No. 0.0071;
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                                                                                                                                                                                                                                                                                                                                                                          Version #1.25
                DB 4;
0.0071;
                               Length 85
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   Indels
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PCT-US95-17111A-92/c
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                                                                                                                                                                                               Sequence 91, Application US/08454557C Patent No. 5830670
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                           GENERAL INFORMATION:
APPLICANT: de la Monte, S
APPLICANT: Wands, Jack R.
                                                                                                                                                                                                                                                                                                                               21802 CGGGCGGATCACGAGGTCAGGAGATCGAGACCATC 21836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 06
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 85 base pairs
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA: APPLICATION NUMBER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                       CORRESPONDENCE ADDRESS:
                                                                                        TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease NUMBER OF SEQUENCES: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                         48 CGGGCGGATCACGAGGTCAGGAGATCGAGACCATC 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: 1
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A. ZIP: 20005-3934
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                                                      ADDRESSEE:
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Washington D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
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                                   Sterne, Kessler, Goldstein & Fox P.L.L.C
1100 New York Avenue, Suite 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             both
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                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
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                                                                                                                                                               Suzanne
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                                                                                                                                                                                                                                                                                                                                                                                                   Score 35; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                   DB 6;
. 0.0071;
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COUNTRY:

RY: U.S.A. 20005-3934

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APPLICATION NUMBER: US/08/454
FILING DATE: 30 MAY-195
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: LUGWIS, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
INFORMATION FOR 55Q ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
US-08-454-557C-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
US-08-340-426D-91
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET MUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEPAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 84 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                            COUNTRY: U.S.A.
COUNTRY: U.S.A.
ZIP: 2005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,426D
FILING DATE: 14-NOV-1994
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: I.SELOGO B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 0.1%; Score 34; DB 3; Lv
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 34; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 91, Application US/08340426D Patent No. 5948634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           atent No. 5948634
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA REPLECATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Sterne, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1100 New CITY: Washington STATE: D.C.
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US-08-450-673C-91
                                                                                                           Search completed: March 30, 2000, 10:42:50 Job time: 111232 sec
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Patent No. 5
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SEQUENCE CHARACTERISTICS:

LENGTH: 84 base pairs

TYPE: nucleic acid

TYPES: nucleic both

STRANDEDNESS: both

TOPOLOGY: both

US-08-450-673C-91
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COMPUTER READABLE FORM:

MEDIUM TYPE: Flopy disk

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTMARE: Patentin Release #1.0, Version #1.25

SOFTMARE: PATENTION DATA:

APPLICATION NUMBER: US/08/450,673C

FILING DATE: 30-MAY-1995

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: LIGHTS, Steven R.
                                                                                                                                                                    Query Match
Best Local Similarity
Matches 34; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 0.1%; Sometimes 0.
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                                                 2676 GCCCGCCTCAGCCTCCCAAAGTGCTGGGATTACA 2709
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REGISTRATION UNMBER: 36,203
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: bo
44 GCCCGCCTCAGCCTCCCAAAGTGCTGGGATTACA 77
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20005-3934
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ative 0; Mismatches
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13817.943 Million cell updates/sec
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R07384 ye96c03.rl
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ACCESSION
VERSION
KEYWORDS
SOURCE
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R07384
LOCUS
DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The WashU-Merck EST Project.
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 83)
11(bases 1 to 83)
11(lar,L., Clark,M., Dubuque,T., Elliston,K., Hawkins,M., Hillier,L., Clark,M., Dubuque,T., ElM., Lennon,G., Marra,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Parsokis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                            R07384 83 bp
ye96c03.rl Soares fetal
IMAGE:125572 5' similar
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AA072757
AI032967
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AD5515337
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BA656150
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BA6561616
                                                                                                                                                                                                                                                                                                                                                          mRNA 05-APR-1995
liver spleen lNFLS Homo sapiens cDNA clone
to gb:x57130_cds1 HISTONE H1D (HUMAN);,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
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AA280198 zt04b12 s
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F29274 HSPD19064
AA457423 aa86b02 r
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                                                                                                                                                                        TITLE
JOURNAL
COMMENT
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VERSION
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AA780764/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
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Best Local Similarity 100.0%; P
Matches 54; Conservative 0;
                                                                                                                                                                                                                                                                                       AUTHORS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E Likaryota; Methazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 91)

K Illier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Marrin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Thesising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. WashU-NCI human EST Project

On Sep 12, 1996 this sequence version replaced gi:1407381.

Contact: Wilson RK.

WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1810

Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (Anfodimage.linl.gov) for further information.

Seq primer: -40m13 fwd. ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA780764 91 bp mRNA EST 05-FEB-1998 ac68f12.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone INAGE:867791 3' similar to contains Alu repetitive element;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
Insert Size: 806
High qailty sequence starts: 1 High qailty sequence stops: 1
Source: IMAGE Consortium, LLNL This clone is available royalty-free
through LLNL; contact the IMAGE Consortium (info@image.llnl.gov)
for further information. Trace considered overall poor quality
Insert Length: 806
Std Error: 0.00
Seq.primer: M13RP1
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Location/Qualifiers
1. 83
                                                                                                                                                                                                                                                                                                                                                                                 human.
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AA780764
AA780764.1 GI:2840095
AA780764.1
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Fax: 314 286 1810
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/db_xref="GDB:478117"
/db_xref="taxon:9606"
/clone="IMAGE:125572"
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/sex-"male"
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zt04b12.rl |
similar to
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Insert Length: 622 Std Error: 0.00
Seq primer: -28ml3 rev2 ET from Amersham.
                                                                                                                                                                                                                                                                                                                                            Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Putative full length read
                                                                                                                                                                                                                                                                                                                                                                                                            On Sep 12, 1996 this sequence version replaced g1:1395022 Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/clone="IMAGE:867791"
/clone_lib="Stratagene fetal retina 937202"
                                                                                                                                                                     /tissue_type="germinal center B cell"
/lab_host="DH10B"
                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                       /clone_lib="NCI_CGAP_GCB1"
                                                                                                                                                                                                                    /clone="IMAGE:712127"
                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98 bp mRNA EST 14-AUG-1997
NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712127 5'
contains Alu repetitive element;contains element MER22'
element ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GI:1921755
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Eco RI sites of the modified pT/T3 vector. Library
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Pred. No.
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3.1e-06;
hes 0;
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                                                                              Query Match
Best Local
                                                              Matches
              13081 GTGCAAACGAAAGGCACCGGTGCTTCTGGCTCCTTTAAACTCAACAAGAAGGC 13133
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73

GTGCAAACGAAAGGCACCGGTGCTTCTGGCTCCTTTAAACTCAACAAGAAGGC

Local

Similarity

0.2%;

Score 53; Pred. No. Mismatches

DB 42; 1 2.9e-06; ches 0;

Length 100;

Indels

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Conservative

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AUTHORS
TITLE
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AI077628/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL; MAGE Consortium (info@image.llnl.gov) for further i Trace considered overall poor quality Insert Length: 820 Std Error: 0.00 Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
On Jan 19, 1998 this sequence version replaced gi:2153436
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
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1 (bases 1 to 100)

NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
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AI077628
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a 25 c 33 g 15 t
           double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo."

28 c 28 g 28 t
                                                                                                                                                                                              /tissue_type="senescent fibroblast"
/lab_host="DH10B (ampicillin resistant)"
/note="vector: pT7T3D (Pharmacia) with a modified
/note="vector: pT7T3D (Pharmacia) with a modified
polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: Eco
RI; 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5'
                                                                                                                                                  /organism-"Homo sapiens"
/db_xref-"taxon:9606"
/clone-"TMAGE:1666975"
/clone_lib-"Soares_senescent_fibroblasts_NbHSF"
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AQ319270/c
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AQ319270
AQ319270.1 GI:4052235
GSS.
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1 (Dases 1 to 102)

1 (Dases 1 to 102)

Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Badams, M.D., Rounsley, S., Wahle, C., de Jong, P. and Venter, J.C. Berry, K., Granger, D., Suh, E., Wahle, C., de Jong, P. and Venter, J.C. Use of human BAC End Sequences for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQ319270 102 bp DNA GSS 06-MAY-1999
RPCII1-98B22.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-98B22,
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 91)
Lanfranchi,G., Muraro,T., Caldara,F., Pacchioni,B., Pallavicini,A., Pandolfo,D., Toppo,S., Trevisan,S., Scarso,S. and Valle,G.
                                                                                                                                                                                            F29274 91 bp mRNA EST 13-MAY-1999
HSPD19063 HM3 Homo sapiens cDNA clone s4000074G04, mRNA sequence.
F29274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the purchased from pieter@dejong.med.buffalo.edu). Clones may be purchased from Research (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq_primer: Sp6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of human BAC End Sequence Unpublished (1998)
Other_GSSs: RPCIll-98B22.TV
                                                                                                       Homo sapiens
                                                                                                                                                                      F29274.1
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Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Shaying Zhao, William Nie:
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism-"Homo sapiens"
/db_xref-"GDB:7537293"
/db_xref-"taxon:9606"
/clone-"RPCI-11-98B22"
/clone-11b-"RPCI-11"
/sex-"Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /Gell_type="Lymphocytes"
/Gell_type="Lymphocytes"
/note="Vector: pBAC63.6; Site_1: EcoRI; Site_2:
RPCI11 Human Male BAC 1.6; Tary"
1 28 c 31 g 17 t
                                                                                                                                                                      GI:4814900
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Pred. No. 0.00084;
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Dictyostelium discoideum

Dictyostelium discoideum

Eukaryota; Dictyosteliida; Dictyostelium.

1 (bases 1 to 93)

Norio, T., Urushihara, H., Saito, T., Ugawa, Y., Mizuno, H., Yoshida, Yoshino, R., Mitra, B.N., Pi, M., Sato, T., Takemoto, K., Yasukawa, H. Yoshino, R., Mitra, B.N., Pi, M., Sato, T., Takemoto, K., Yasukawa, H. Williams, J., Waeda, M., Takeuchi, I., Ochiai, H. and Tanaka, Y. The Dictyostelium developmental cDNA project: generation and analysis of expressed sequence tags from the first-finger stage
                                                              On Dec 5, 1997 this sequence version replaced Contact: Hideko Urushihara Institute of Biological Sciences University of Tsukuba 3-3-10 Ten-nodal, Tsukuba, Ibaraki 305, Japan Email: d402hu@sakura.cc.tsukuba.ac.to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 0.1%; Score 43; l Similarity 100.0%; Pred. No. 43; Conservative 0; Mismatci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identification of 4370 expressed sequence tags from a 3'-end-specific cDNA library of human skeletal muscle by sequencing and filter hybridization genome Res. 6 (1), 35-42 (1996) 96276048 on Apr 7, 1998 this sequence version replaced g1:3034419. Contact: Valle G.
                                                                                                                                                                                         DNA Res. 5 (6), 335-340 (1998)
99156227
                                                                                                                                                                                                                                   development
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EST.
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ABI Chromatograms and
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                                             d402hu@sakura.cc.tsukuba.ac.
T = 'Dictyostelium discoideum
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/db_xref="taxon:9606"
/clone="84000074604"
/clone_llb="HM3"
/sex="female"
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Location/Qualifiers
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.cDNA project in Japan'.
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g1:2662913

Yasukawa, H.,

Yoshida, M.,

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REFERENCE
AUTHORS
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SOURCE
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AA457423/c
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Matches 43
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JOURNAL
                                  26294 TCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATGGCGTGAAC 26335
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nes 43; Conservat
l Similarity
42; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. See primer: -28ml3 rev1 Er from Amersham High quality sequence stop: 76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 95)
Hiller, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylle, T., Waterston, R. and Wilson, R. Washu-Merck EST Project 1997
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA457423 95 bp mRNA EST 06-JUN-1997 aa86b02.rl Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:838155 5' similar to contains Alu repetitive element;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On Nov 4, 1996 this sequence version replaced gi:1671271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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llarity 100.0%;
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                                                                                                                                                                                                                                                                                                                      /note-"Vector: pBluescript SK-; Site_1: EcoRI; Site_2: xhoI; Cloned unidirectionally. Primer: Oligo dT. Pooled retinal tissue. Average insert size: 10.6kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTOGCACGAG 3' -3' adaptor sequence: 5' CTGGAGTTTTTTTTTTTTTTTTT 3'" 3 of 25 g 17 t
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/strain="AX4"
/db_xref="taxon:44689"
/clone="SSH729"
/clone=lib="Dictyostelium discoideum
/dev_stage="slug"
2 c 1 g 33 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:838155"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /lab_host="SOLR (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Stratagene fetal retina 937202"
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0; Mismatches
                                                                                                       Score 42; DB; Pred. No. 0.(
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                                                                                                                                         DB 34; Length 95; 0.0074;
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KEYWORDS
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Best Local S
Matches 41
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TITLE
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                                                                                                                                                                                                                                                                                                                     ORGANISM
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                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 92)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT = Dictyostelium discoideum cDNA project
Location/Qualifiers
                                                                      Unpublished (1997)
On Dec 20, 1995 this sequence version replaced gi:11341
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AU072757 73 bp mRNA EST 24-JUN-1999
AU072757 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium
discoideum cDNA clone SSA765, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
AI932967
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Unpublished (1999)
On Jun 5, 1998 this sequence version replaced gi:3188495.
Contact: Hideko Urushihara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Dictyosteliida; Dictyostelium 1 (bases 1 to 73) Urushihara, H.
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cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.1%; Score 41; ilarity 100.0%; Pred. No. Conservative 0; Mismatc
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/clone="SSA765"
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/strain="AX4"
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IMAGE:2457833
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FEATURES

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Orber GSSs: CITBI-21-2650p18.TF
Other GSSs: CITBI-21-2650p18.TF
CONTACT: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                            end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
class: BAC ends.
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CITBI-E1-2650P18.TR CITBI-E1 Homo sapiens genomic clone 2650P18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: -40UP from Gibco.
Location/Qualifiers
                                                                                                                                                                                                                                                                      Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 104)
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www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQ626158.1 GI:5088550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 0.1%; Score 41; DB 62; Length 92;
Similarity 100.0%; Pred. No. 0.015;
41; Conservative 0; Mismatches 0; Indels
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/cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
CalTech Human BAC Library D"
28 c 22 g 42 t
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/clone_11b="NCI_CGAP_Gas4"
/tlssue_type="poorly differentiated adenocarcinoma with
signet ring cell_features"
                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2650P18"
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/db_xref="taxon:9606"
                                                                              /sex="male"
                                                                                             /clone_lib-"CITBI-E1"
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3-1 Yamada-oka, S
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SOURCE ORGANISM ACCESSION VERSION KEYWORDS

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COMMENT

JOURNAL

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Query Match 0.1%; Score 41; DB 105; Length 104; Best Local Similarity 100.0%; Pred. No. 0.014; Matches 41; Conservative 0; Mismatches 0; Indels
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1 (bases 1 to 52)

Okubo, K., Yoshii, J., Yokouchi, H., Kameyama, M. and Matsubara, K.
Global analysis of gene expression in colon mucosa: a large scale random cDNA sequencing analysis
Unpublished (1994)
Contact: Okubo, K., Itoh, K., Yoshii, J., Yokouchi, H. and Matsubara, K.
Institute for Molecular and Cellular Biology
Tumor Gene Index Unpublished (1997) on Jan 14, 1998 this sequence version replaced gi:1877755 Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov
                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 97)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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//db_xref="ftaxon:9606"
//clone="cm2335"
/clone=llb="Human colon mucosa"
/note-"Adult male, tissue_type = colon mucosa "
17 c 14 g 9 t
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Use of BAC End Sequences for Sequence-Ready Map Building Unpublished (1997)
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Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 97.
Location/Qualifiers
                     Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 103)
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                                                                                                                                                                                                                                                                                 Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                    Adams,M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and
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/db_xref="taxon:9606"
/clone="IMAGE:1522331"
/clone_lib="NCI_CGAP_Lu5"
/tissue_type="carcinoid"
/lab_host="DH10B"
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Suzuki.K., Shimizu.H. and Urushiihara,H.
Sexual cDNA in D. discoideum(970724)
Unpublished (1997)
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C25772 Dictyostelium discoideum
discoideum cDNA clone FC-BB11, m
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Institute of Biological Sciences
University of Tsukuba
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/note="Vector: pBACe3.6; Site_1:
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     AR051499 76 bp DNA
Sequence 69 from patent US 5830670.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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1 (bases 1 to 76)

1 (bases 1, to 76)

de la Monte, S. and Wands, J.R.

Neural thread protein gene expression and detection of Alzheimer's disease
                                                                                                                                                                                                                                                     Sequence 159 from patent US 5869241.
AR032547
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de la Monte,S. and Wands,J.R.
Neural thread protein gene expression and detection of Alzheimer's
                                                            1 (bases 1 to 48)
Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.l
Edwards of determining DNA sequence preference of a DNA-binding
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US 5869241-A 159 09-FEB-1999;
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19 c 18 g
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                                                                                         y Match 0.2%; Score 48; DB 5; Length 48; Local Similarity 100.0%; Pred. No. 2e-13; hes 48; Conservative 0; Mismatches 0; Indels
     48 GAGAGAATAGGAAACCGATCTTTATATATCTACGTTACCCCCTGCCCCCC
                                                                                                                                                                                                                                                                     Unclassified.

1 (bases 1 to 48)

1 (bases 1 to 48)

Edwards (C.A., Cantor, C.R., Andrews, B.M. and Turin, L.M.

Edwards (C.A., Cantor, C.R., Andrews, B.M. and Turin, L.M.

Screening assay for the detection of DNA-binding molecules

Screening ass
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Sequence 159 from patent US 5578444.
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129287.1 GI:1820078
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Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E.
Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and methods
Sequence-directed DNA-binding molecules compositions and methods
Patent: US 5578444-A 159 26-NOV-1996;
Location/Qualifiers
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1 Similarity 100.0%;
47; Conservative 0;
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Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E.
Sequence-directed DNA-binding molecules compositions and methods
Patent: US 5578444-A 170 26-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 47) Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E. Method of determining DNA sequence preference of a DNA-binding
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Sequence 170 from
AR032558
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Location/Qualifiers
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Best Local Similarity 100.0%;
Matches 46; Conservative
Query Match
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Location/Qualifiers
1. .47
                                                                                                                                                                                                     Sequence
I29295
                                                                                    i (bases 1 to 46)
Edwards,C.A., Cantor,C.R., Andrews,B.M.,
Sequence-directed DNA-binding molecules of
Patent: US 5578444-A 167 26-NOV-1996;
Location/Qualifiers
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Edwards.C.A., Cantor.C.R., Andrews,
Method of determining DNA sequence
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Sequence 167 from
AR032555
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DB 5; Length 46; 2.2e-12;
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                                                                                                             Turin, L.M. and Fry, K.E. compositions and methods
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Db 1 CACAGCCTACCTCCAGTCAGTATAAATACTTCTCTCTCCCTTGCGTTC 46
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Db 1 ATTITTGAATTITCTTGGGTCCAATAGTTGGTGGTCTGACTCTAT 45
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Sequence 167 from patent
190969
190969.1 GI:3935435
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Edwards,C.A., Cantor,C.R., Andrews,B.M. and Turin,L.M.
Screening assay for the detection of DNA-binding molecules
Patent: US 5726014-A 167 10-MAR-1998;
Location/Qualifiers
1. 46
 Sequence 169
129297
                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 45)
Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E. Method of determining DNA sequence preference of a DNA-binding
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                                                                                                                                                 0.1%; Score 45; DB 5; I larity 100.0%; Pred. No. 7.4e-12; Conservative 0; Mismatches 0;
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Sequence 169 from patent
190971
190971.1 GI:3935441
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Edwards,C.A., Cantor,C.R., Andrews,B.M. and Turin,L.M.
Screening assay for the detection of DNA-binding molecules
Patent: US 5725014-A 199 10-MAR-1998;
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Edwards,C.A., Cantor,C.R., Andrews,B.M., Turin,L.M. and Fry,K.E.

Sequence-directed DNA-binding molecules compositions and methods

Patent: US 5578444-A 169 26-NOV-1996;
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 79)
Schichman,S.A., Caligiuri,M.A., Strout,M.P., Carter,S.L., Gu,Y., Canaani,E., Bloomfield,C.D. and Croce,C.M.
ALL-1 tandem duplication in acute myeloid leukemia with a normal karyotype involves homologous recombination between Alu elements Cancer Res. 54 (16), 4277-4280 (1994)
                                                                                                                                                   $73203 79 bp DNP
ALL-1 (tandem duplication)
Genomic Mutant, 79 nt).
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$73203.1 GI:685048
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GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 155288] from the original journal article. This sequence comes from Fig. 3a.

Map location: 11.

Location/Qualifiers
1. 79
9 /organism="Homo sapiens"
/db_xref="taxon:9606"
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Query Match 0.2%; Score 48; DB 1; Le Best Local Similarity 100.0%; Pred. No. 9.7e-05; Matches 48; Conservative 0; Mismatches 0;

Length 48; 5; 1; Indels

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uls method is to where the tar where the tar Jacent to the Jacent to the Jacent to 1731 and Q69 contg. sites) to promoter trandomly gene purposes, e.g and UL9 (see and UL9 (see all 2 A; 8 C;	NA-binding molec as molecular re 587pp; English. 587pp; English to re biologica guences. The as ences can be tes ed protein-bindicest sequences change con the concept to the concept the equili	BP. stone, ta stone, ta ; test se ;; test se ;; transe ;; transe ;; transe ;; transe ;; transe	Q86183 Q86183 T30807 T30807 T35073 T35073 T35073 V42384 V70704 V70704 Q33621 ALIC	V7068
is disturbed, generating changes in the concentration of free one application of this method is to eucaryotic general transge factors (e.g. TFIID), where the target region is typically selferom DNA sequences adjacent to the binding site for the eucary transcription factor. Numerous exemplary test sequences are the sequences in 0609251-731 and 0609850 correspond to promoter (typically, TATA box-contg. sites) for human genes and the seq 0609732-849 correspond to promoter targets for viral genes. The sequences may also be randomly generated. DNA: protein interaction used for screening purposes, e.g. the Herpes Simplex Virus origin of replication and UL9 (see 069851-52, 069865 and 06988 sequence 48 BP; 12 A; 8 C; 14 G; 14 T;	ylence-directed DNA-binding molecules - useful in simaceuticals and as molecular reagents iim 28; Page 291; 587pp; English. NA protein binding assay is provided, useful for screening staries of synthetic or biological cpds. for their ability bind DNA test sequences. The assay is versatile in that any bind DNA test sequences can be tested by placing the test sequence placent to a defined protein-binding screening sequence. Binding mols. to these test sequences changes the binding characteristics the protein mol. to its cognate binding sequence. When such a mol sthe test sequence, the equilibrium of the DNA:protein complexes	ne, target region. est sequence; screening sequerses Simplex Virus; HSV; transcription factor; TFIID: transcription factor; TFIID:	NMENTS	
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CC The sequences given in T63713-4312 represent duplex DNA's which act CC as target regions in the method of the invention. The method for CC altering the binding characteristics of a DNA-binding protein to duplex DNA comprises contacting the duplex DNA with a small molecule which CC DNA comprises contacting the duplex DNA with a small molecule which CC DNA comprises contacting the duplex DNA with a small molecule which CC molecule is bound to the target region, it is adjacent to, but not converlapping by more than 4 bp, a binding site for a DNA-binding protein. CC The small molecule is added at a concentration effective to alter the CC binding of the DNA binding protein, pref. TFIID, to its binding site on the duplex DNA. The binding protein to its binding site. The CC compounds isolated using this method are potentially useful as CC the binding of the DNA-binding protein to its binding site. The CC compounds isolated using this method are potentially useful as CC the method is suitable for scenening large biological or chemical CC The method is suitable for screening large biological or chemical CC interaries and allows determination of sequence-specific and relative CC affinities of known DNA-binding agents for different DNA sequences. CC The design of these duplex DNA's allows a single DNA:protein interaction CC to be used for screening sequence-specific, or preferential, DNA binding CC proteins that recognise almost any possible sequence (see also T49539-CC T4).
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Matches 48
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27-JUN-1991; US-723618.
23-DEC-1992; US-996783.
17-SEP-1993; US-123936.
20-DEC-1993; US-171389.
                                                                  Homo sapiens.
US5869241-A.
09-FEB-1999.
07-JUN-1995.
20-DEC 1993.
27-JUN-1991.
23-DEC-1992.
U17-SEP-1993.
U7-JUN-1995.
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US5578444-A.
26-NOV-1996.
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Andrews BM, Cantor CR, Edwards CA, Fry KE, Turin LM;
WPI; 97-020402/02.
Altering binding characteristics of DNA binding proteins to duplex
DNA - by attaching specific small cpd. to target region close to the
protein's binding site, useful in treatment of viral disease, cancer
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Duplex NBA; target region; binding characteristic; DNA binding protein;

TFIID; transcription factor; binding site; inhibition; enhance;

cancer; inherited genetic disorder; alpha-D-galactosidase A; ds.
                                                                                                                                                                                                                                                                                                                                                     Test sequence from human H4/a gene for H4 histone. Test sequence; DNA-binding molecule; screening sequenceic acid amplification; target; viral; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9/c
X17159 standard; DNA; 48 BP
       Andrews
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N-1995; 475228.

N-1993; US-171389.

N-1993; US-926783.

N-1993; US-996783.

N-1993; US-123936.

N-1995; US-475228.

N-1995; US-475228.

N-1995; US-475228.

N-1995; US-475228.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 0.2%;
Similarity 100.0%;
48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      997 (first entry)
/a gene (for Histone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 48; DB 1; Le
Pred. No. 9.7e-05;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14 G;
       Turin LM
                                                                                                                                                                                                                                                                                                                                                                                              sequence; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14
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DR WPI, 99-15755/13.

PRESENTINGLEMON EDWA Sequence preference of a DNA-binding molecula - PT beginns attained to test sequence process to oligonucleotide process and trained to test sequence process to oligonucleotide process and trained to test sequence process and trained to test sequence process and trained to test sequence process and trained to test sequences x17001 to x1600 represent specifically claimed target test concentration of the process and trained to the method of the invention of the mixture of claim 3; Columns 181-182; 270pp; Baptista Company to the process and trained that are used in the method of the invention of the mixture of claims and the process of the concentration o
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                                                                                                                                                                                                          The sequences given in 763713-4312 represent duplex DNA's which act CC as target regions in the method of the Invention. The method for CC altering the binding characteristics of a DNA-binding protein to duplex CDNA comprises contacting the duplex DNA with a small molecule which comprises contacting the duplex DNA with a small molecule which comprises contacting the duplex DNA with a small molecule which conclecule is bound to the target region, where, when the small coverlapping by more than 4 bp, a binding site for a DNA-binding protein. The small molecule is added at a concentration effective to alter the binding of the DNA binding protein, pref. TFIID, to its binding site on the duplex DNA. The binding protein to its binding site on the duplex DNA, The binding of the small molecule may inhibit or enhance the binding of the DNA-binding protein to its binding site. The CC compounds isolated using this method are potentially useful as CC therapeutic agents for treatment of any disease which involves a CC specific DNA sequence, e.g. cancer, or inherited genetic disorders etc. The method is suitable for screening large biological or chemical CC libraries and allows determination of sequence-specific and relative affinities of known DNA-binding agents for different DNA sequences. CC The design of these duplex DNA's allows a single DNA:protein interaction to be used for screening sequence-specific, or preferential, DNA binding contents that recomplies almost any possible sequences.
                                                                      Query Match
Best Local S
Matches 47
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Best Local
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27-JUN-1991; 723618.
27-JUN-1991; US-723618.
27-JUN-1991; US-996783.
23-DEC-1992; US-996783.
17-SEP-1993; US-123936.
20-DEC-1993; US-171389.
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                                   12078
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Human H3 histone gene TFIID binding site.
Buplex DNA; target region; binding characteristic; DNA binding protein;
TFIID: transcription factor; binding site; inhibition; enhance; hCG;
cancer; inherited genetic disorder; alpha-D-galactosidase A; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequences may also be
be used for screening
origin of replication
Sequence 47 BP; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; Column 185-186; 264pp; E
The sequences given in T63713-431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Altering binding characteristics of DNA binding proteins to duplex DNA - by attaching specific small cpd. to target region close to the protein's binding site, useful in treatment of viral disease, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GENE-) GENELABS TECHNOLOGIES INC. Andrews BM, Cantor CR, Edwards CA, WPI; 97-020402/02.
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                                                                                                                                                               Sequence
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CAATAGTTGGTGGTCTGACTCTATAAAAGAAGAGTAGCTCTTTCCTT
                  CAATAGTTGGTGGTCTGACTCTATAAAAGAAGAGTAGCTCTTTCCTT 12124
                                                                      0.2%;
l Similarity 100.0%;
47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
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47; Conser
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                                                                                                                                                               BP;
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13 A; 8 C; 10 G; 16 T;
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                                                                      Score 47; DB; Pred. No. 0.0
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Pred. No.
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                                                                DB 1;
,. 0.00018;
0;
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0.0001
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                                                                                                                                                                                                   sequence
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                                                                                                      Length 47
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                                                                       Indels
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so T49539-
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Pr Sequence attached to test sequence

Pr Claim 3; COLumns 187-188; 270pp; English.

CC Sequences X17001 to X17600 represent specifically claimed target test sequences that are used in the method of the invention of determining the CC DNA sequence preference of a DNA-binding protein to a mixture of duplex DNA test oligonucleotides, each of the test oligonucleotides (1) adding a test molecule and a DNA-binding protein to a mixture of duplex DNA test sequence adjacent to a screening sequence, where the screening sequence binds to the DNA-binding protein with a binding called the test sequence, (ii) incubating the test molecule, the mixture of duplex DNA test oligonucleotides includes several test sequences; (ii) incubating the test molecule, the mixture of duplex DNA test oligonucleotides includes several test sequences; (iii) incubating the test molecule, the mixture of duplex DNA test oligonucleotides includes several test sequences and the DNA-binding protein for a time considered that the permit binding of the test molecule, the mixture of duplex DNA; (iii) separating unbound test oligonucleotides from test coligonucleotides bound to binding protein; (iv) amplifying the unbound test oligonucleotides. (v) repeating steps (ii) to (iv); (v) isolating the amplified test oligonucleotides; and (vii) sequencing the isolated test oligonucleotides. Test sequences X17481 and X17600 correspond to promoter targets for viral genes.

Sequence X17482-X17599

Sequence 47 BP; 13 A; 8 C; 10 G; 16 T;
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Best Local Similarity
Matches 47; Conser
W09414980-A.
07-UIL-1994.
20-DEC-1993; UIZ-388.
23-DEC-1992; US-996783.
17-SEP-1993; US-123936.
(GENE-) GENELABS TECHNOLOGIES I
Andrews BM, Cantor CR, Edward
WPI; 94-234711/28.
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20-DEC-1993; US-171389.
27-JUN-1991; US-723618.
23-DEC-1992; US-996783.
17-SEP-1993; US-123936.
07-JUN-1995; US-475228.
(GENE-) GENELABS TECHNOLOGIES INC.
Andrews BM, Cantor CR, Edwards CA, F.
WPI; 99-152755/13.
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                                                                                                                                                                                                                                                                                                                                                                                       Human H2a histone gene,
DNA protein-binding ass
promoter; target; TATA
origin of replication;
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Test sequence; DNA-binding molecule; screening sequence;
nucleic acid amplification; target; viral; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q69417 standard;
Q69417;
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09-FEB-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     assay;
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                                                                                                                                                                                                                                                                                                                                                                                                tox;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             target region
                                                 OGIES INC.
Edwards CA,
                                                                                                                                                                                                                                                                                                                                                                                            test sequence; screening sequence;
; Herpes Simplex Virus; HSV;
; transcription factor; TFIID: ds.
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0.000
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s 0;
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RESULT
T63879
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PS Claim 28; Page 295; 587pp; English.
CC laim 28; Page 295; 587pp; English.
CC libraries of synthetic or biological cycle, for their ability
CC libraries of synthetic or biological cycle, for their ability
CC number of test sequences. The assay is versatile in that any
CC number of test sequences can be tested by placing the test sequence
CC adjacent to a defined protein-binding screening sequence. Binding
CC of mols to these test sequences changes the binding characteristics
CC of the protein mol not its cognate binding sequence. When such a mol
CC of the protein mol not its cognate binding sequence. When such a mol
CC of the protein of this method is to encaryotic general transcription
CC one application of this method is to encaryotic general transcription
CC factors (e.g. TFIID), where the target region is typically selected
CC from DNA sequences adjacent to the binding site for the encaryotic
CC transcription factor. Numerous exemplary test sequences are given:
CC the sequences in 069251-731 and 069850 correspond to promoter targets
CC (typically, TATA box-conty, sites) for human genes and the sequences in
CC sequences may also be randomly generated. DNA:protein interaction may
CC origin of replication and UJ9 (see 050851-52, 069865 and 069891).
SQ Sequence 46 BP; 10 A; 16 C; 6 G; 14 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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The sequences given in T63713-4312 represent duplex DNA's which act as target regions in the method of the invention. The method for altering the binding characteristics of a DNA-binding protein to duplex DNA comprises contacting the duplex DNA with a small molecule which binds sequence-specifically to a target region, where, when the small molecule is bound to the target region, it is adjacent to, but not overlapping by more than 4 bp, a binding site for a DNA-binding protein. The small molecule is added at a concentration effective to alter the binding of the DNA binding protein, pref. TFIID, to its binding site on the duplex DNA. The binding of the small molecule may inhibit or enhance the binding of the DNA-binding protein to its binding site. The compounds isolated using this method are potentially useful as therapeutic agents for treatment of any disease which involves a specific DNA sequence, e.g. cancer, or inherited genetic disorders etc.
                                                                                                                                                                                                                                                                                                                                                                              26-NOV-1996.
27-JUN-1991; 723618.
27-JUN-1991; US-723618.
23-DEC-1993; US-996783.
17-SEP-1993; US-123936.
17-SEP-1993; US-121398.
(GENE-) GENELABS TECHNOLOGIES INC.
Andrews BM, Centor CR, Edwards CA, Fry KE, Turin LM;
April 97-020402/02.
Altering binding characteristics of DNA binding proteins to duplex
DNA - by attaching specific small cpd. to target region close to the
DNA - by attaching specific small cpd. to target region close to the
DNA - by attaching specific small cpd. to target region close to the
DNA - by attaching specific small cpd. to target region close to the
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T63879;
14-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human H2a histone gene TFIID binding site.

Duplex DNA; target region; binding characteristic; DNA binding protein;

TFIID; transcription factor; binding site; inhibition; enhance; hCG;

cancer; inherited genetic disorder; alpha-D-galactosidase A; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
US5578444-A.
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ilarity 100.0%;
Conservative
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Pred. No.
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Matches

Local

ch 0.2%; l similarity 100.0%; 46; Conservative

0 Score 46; Pred. No.

Mismatches

DB 1;

Length 46;

00034;

Indels

0, Gaps

0

Qy . 10562 CACAGCCTACCTCCAGTCAGTATAAATACTTCTCTGCCTTGCGTTC 10607

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PT Determination of DNA sequence preference of a DNA-binding molecule - PT based on inhibition of binding of protein to oligonucleotide PT sequence attached to test sequence PS Claim 3; Columns 185-186; 270p; English.

CC Sequences X17001 to X17600 represent specifically claimed target test CC sequences X17001 to X17600 represent specifically claimed target test CC plays sequence preference of a DNA-binding molecule. The method comprises: CC (1) adding a test molecule and a DNA-binding protein to a mixture of CC duplex DNA test oligonucleotides, each of the test oligonucleotides can be comprised to a screening sequence binds to the DNA-binding protein with a binding CC and where the mixture of duplex DNA test oligonucleotides includes can deviate the mixture of duplex DNA test oligonucleotides includes can deviate the mixture of duplex DNA test oligonucleotides and the DNA-binding protein for a time complex DNA; (11) separating unbound test oligonucleotides from test oligonucleotides and the DNA-binding protein for a time confidence of the sequence of the sequences in class oligonucleotides; (v) repeating steps (ii) to (iv); (vi) isolating the sequence oligonucleotides; (v) repeating steps (ii) to (iv); (vi) isolating the analytical test oligonucleotides; (v) repeating steps (ii) to (iv); (vi) isolating contest oligonucleotides; (v) repeating steps (ii) to (iv); (vi) isolating the solated contest oligonucleotides. Test sequences x17481 and x17500 correspond to promoter targets for vital genes.

Sequence 46 BP; 10 A; 16 C; 6 G; 14 T;
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Best Local S
Matches 46
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07-JUN-1995; 475228.

20-DEC-1993; US-171389.

27-JUN-1991; US-723618.

27-JUN-1991; US-966783.

17-SEP-1993; US-475278.

07-JUN-1995; US-475228.

(GENE-) GENELABS TECHNOLOGIES INC.

ANDREWS BM. CANTOX CR. EDWARDS CA. FT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The method is suitable for screening large biological or chemical libraries and allows determination of sequence-specific and relative affinities of known DNA-binding agents for different DNA sequences. The design of these duplex DNA's allows a single DNA:protein interaction to be used for screening sequence-specific, or preferential, DNA binding proteins that recognise almost any possible sequence (see also T49539-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-MAY-1999 (first entry)
Test sequence from human histone H2a gene.
Test sequence; DNA-binding molecule; screening sequence; human; nucleic acid amplification; target; viral; ds.
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X17167;
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Pred. No.
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.00034;
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RESULTANTA DE LA COLOR DE LA C
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T63881
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PS Claim 28; Page 296; 587pp; English.

CC A DNA protein-binding assay is provided, useful for screening

CC libraries of synthetic or biological cpds. for their ability

CC number of test sequences. The assay is versatile in that any

CC number of test sequences can be tested by placing the test sequence

CC adjacent to a defined protein-binding screening sequence. Binding

CC of mols. to these test sequences changes the binding characteristics

CC of the protein mol. to its cognate binding sequence. When such a mol.

CC of the protein mol. to its cognate binding sequence. When such a mol.

CC of the protein mol. to its cognate binding sequence. When such a mol.

CC on application of this method is to eucaryotic general transcription

CC factors (e.g. TFIID), where the target region is typically selected

CC transcription factor. Numerous exemplary test sequences are given:

CC the sequences in 069251-731 and 069850 correspond to promoter targets

CC (typically, TATA box-conty, sites) for human genes and the sequences in

CC sequences may also be randomly generated. DNA:protein interaction may

CC origin of replication and UL9 (see 069851-52, 069865 and 069891).

SQ Sequence 45 BP; 8 A; 6 C; 10 G; 21 T;
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Best Local Similarity
Matches 45; Conser
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                                                                              26-NOV-1996.
27-JUN-1991; 723618.
27-JUN-1991; US-723618.
27-DEC-1992; US-996783.
17-SEP-1993; US-123936.
20-DEC-1993; US-171389.
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17-SEP-1993; US-123936.
(GENE-) GENELABS TECHNOLOGIES INC.
Andrews BM. Cantor CR, Edwards CA,
WPI: 94-234711/28.
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Human H3 histone gene, target region.
Human H3 histone gene, target region.
DNA protein-binding assay; test sequence; screening sequence;
promoter; target; TATA box; Herpes Simplex Virus; HSV;
origin of replication; UL9; transcription factor; TFIID: ds.
                                                                                                                                                                                                                                                                      US5578444-A.
                                                                                                                                                                                                                                                                                                                  Human H3 histone gene TFIID binding site.

Buplex DNA; target region; binding characteristic; DNA binding protein;

TFIID; transcription factor; binding site; inhibition; enhance; hCG;

cancer; inherited genetic disorder; alpha-D-galactosidase A; ds.
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                        Andrews
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                                                     (GENE-)
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                     BM, Cantor CR, Edwards CA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequences given in T63713-4312 represent duplex DNA's which act CC as target regions in the method of the invention. The method for CC altering the binding characteristics of a DNA-binding protein to duplex CC DNA comprises contacting the duplex DNA with a small molecule which binds sequence-specifically to a target region, where, when the small conclude is bound to the target region, where, when the small coverlapping by more than 4 bp, a binding site for a DNA-binding protein. The small molecule is added at a concentration effective to alter the binding of the DNA binding protein, pref. TFIID, to its binding site on the duplex DNA. The binding protein to its binding site on the duplex DNA. The binding protein to its binding site. The compounds isolated using this method are potentially useful as compounds isolated using this method are potentially useful as compounds isolated using this method are potentially useful as compounds isolated using this method are potentially useful as compounds isolated using this method are potentially useful as compounds isolated using this method are potentially useful as compounds isolated using this method are potentially useful as compounds isolated using this method are potentially useful as compounds isolated using this method are potential involves a compound of the sequence, e.g. cancer, or inherited genetic disorders etc. The method is suitable for screening large biological or chemical continues and malanged for screening large biological or chemical continues of known DNA-binding agents for different DNA sequences.

CC therefore the binding sequence-specific and relative affinities of known DNA-binding agents for different DNA sequences.
Determination of DNA sequence preference of a DNA-binding molecule of abased on inhibition of binding of protein to oligonucleotide sequence attached to test sequence? Sequence attached to test sequence sequences x17001 to x17600 represent specifically claimed target test sequences x17001 to x17600 represent specifically claimed target test sequences x17001 to x17600 represent specifically claimed target test sequences that are used in the method of the invention of determining the DNA sequence preference of a DNA-binding molecule. The method comprises:

(1) adding a test molecule and a DNA-binding protein to a mixture of duplex DNA test oligonucleotides, each of the test oligonucleotides having a test sequence adjacent to a screening sequence, where the screening sequence binds to the DNA-binding protein with a binding affinity that is independent of the DNA-binding protein with a binding and where the mixture of duplex DNA test oligonucleotides includes several test sequences; (11) incubating the test molecule, the mixture of duplex DNA test oligonucleotides includes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 45
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07-JUN-1995: 475228.

20-DEC-1993: US-171389.

27-JUN-1991: US-723618.

23-DEC-1992: US-96783.

17-SEP-1993: US-123936.

07-JUN-1999: US-475278.

07-JUN-1999: US-475278.

(GENE-) GENELARS TECHNOLOGIES INC.

ANDREWS BM, Cantor CR, Edwards CA, Fry KE, Turin LM;

WPI: 99-152755/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Altering binding characteristics of DNA binding proteins to duplex DNA - by attaching specific small cpd. to target region close to the protein's binding site, useful in treatment of viral disease, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Test sequence from human histone H3 gene.
Test sequence; DNA-binding molecule; screening sequence; human;
nucleic acid amplification; target; viral; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
US5869241-A.
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l Similarity 100.0%;
45; Conservative (
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0.00065;
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RESULT 13
Q62216/C
ID Q62216 standard; DNA; 30 BP.
AC Q62216
DT 22.00V-1994 (first entry)
DE Histone H3 mRNA probe #1.
KW probe; histone; H2b; H3; H4; m
KW diagnosis; cancer; carcinogen;
OS Synthetic.
PN W09408046-A.
PD 14-APR-1994
PD 14-APR-1994
PD 14-APR-1993; G81977.
PR 02-OCT-1992; GB-020777.
PR 02-OCT-1992; GB-020777.
PR 02-OCT-1993; G01977.
PR 02-OCT-1993; G01977.
PR 02-OCT-1993; G01977.
PR 02-OCT-1993; GB-020777.
PR 02-OCT-1994; GB-020777.
PR 02-OCT-1993; GB-020777.
PR
  RESULT 1
Q62217/c
ID 201622
AC Q622-AC Q622
AC W Proble
KW Proble
KW Proble
KW G1ag
PD 11a-2
PF 20-5
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Best Local Similarity
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Best Local Similarity
Matches 45; Conserv
22-NOV-1994 (first entry)
Histone H3 mRNA probe #2.
Probe; histone; H2b; H3; H4; mRNA; de diagnosis; cancer; carcinogen; ss.
Synthetic.
WC9408046-A.
14-APR-1994.
20-SEP-1993; G01977.
                                                                                                                                                                                                                                                                                                                                                                                                          12518 CGAGTGACTATTATGCCCAAAGACATCCAG 12547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12057 ATTTTTGAATTTTCTTGGGTCCAATAGTTGGTGGTCTGACTCTAT 12101
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Sequence 45 BP; 8 A; 6 C; 10 G; 21 T;
                                                                                                                                                                                                           Q62217 standard; DNA; Q62217;
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Probe; h1stone: H2b; H3; H4; mRNA; detection; proliferation;

Probe; h1stone: carcinogen; ss.
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; Pred. No. 0.00065;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                              detection; proliferation; cell;
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B
                                                                                                                                      Detecting proliferating cells in tissue or cell samples - by probes specific for histone manh for probes specific for histone manh for the sequences given in 062216-18 are probes which are specific for histone H3 mRNA. These probes may be used in the method of the invention for detecting the presence of proliferating cells in a invention for detecting the presence of proliferating the tissue/cell sample. The method comprises preparing the tissue/cell cample, hybridising these non-radioactively labelled probes, and detecting the presence of histone-probe hybrids. The method can be used to identify cells undergoing proliferation in normal and diseased tissue. It can be used in the diagnosis of cancers and in assessing the carcinogenic properties of a chemical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          problem specific for histone many habelled oligonucleotide problem specific for histone many.

Claim 13; Page 18; 24pp; English.

Chistone H3 mRNA. These probes may be used in the method of the invention for detecting the presence of proliferating cells in a cinvention for detecting the presence of proliferating the tissue/cell sample. The method comprises preparing the tissue/cell sample, hybridising these non-radioactively labelled probes, and detecting the presence of histone-probe hybrids. The method can be used to identify cells undergoing proliferation in normal and diseased tissue. It can be used in the diagnosis of cancers and in assessing the carainogenic properties of a chemical.

Seguence 30 BP; 7 A; 7 C; 8 G; 8 T;
                                                              Matches
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Best Local Similarity
                                                                             Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                               14-APR-1994;
20-SEP-1993; G01977.
02-OCT-1992; GB-020777.
(UYLE-) UNIV LEICESTER.
PTING16 JH;
WPI; 94-135606/16.
                  12177 GTACTAAACAGACAGCTCGGAAATCCACCG 12206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12330 GCTACCAAAAGTCGACCGAGTTGCTGATTC 12359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Histone H3 mRNA probe #3.

Probe; histone; H2b; H3; H4; mRNA; detection; proliferation; cell; diagnosis; cancer; carcinogen; ss.

Synthetic.
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Q62218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
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30 GTACTAAACAGACAGCTCGGAAATCCACCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; DNA;
                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.1%; Silarity 100.0%; Conservative 0;
                                                              Conservative
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LEICESTER.
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Pred. No.
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Pred. No.
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Search completed: March 30, 2000, 17:38:54 Job time: 136132 sec



Run

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Result
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Perfect score:
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Maximum DB
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1: /cgn2_6/ptodata/
2: /cgn2_6/ptodata/
3: /cgn2_6/ptodata/
4: /cgn2_6/ptodata/
5: /cgn2_6/ptodata/
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7: /cgn2_6/ptodata/
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length: 105
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Match
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1 TGGCCAGCTGCAGGTGGCGG......TATTCTAAGCCATGGTCAAT 30001
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   GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
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/cgn2_6/ptodata/1/ina/5D_COMB.seq:*
/cgn2_6/ptodata/1/ina/5D_COMB.seq:*
/cgn2_6/ptodata/1/ina/5D_COMB.seq:*
/cgn2_6/ptodata/1/ina/6ackfiles1.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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PCT-US95-17111A-69
US-08-444-557C-57
US-08-450-673C-57
PCT-US95-17111A-57
US-08-171-389-159
US-08-171-389-159
US-08-475-228A-159
US-08-171-389-170
US-08-171-389-170
US-08-171-389-170
US-08-18-2-28A-170
US-08-171-389-170
US-08-171-389-167
US-08-171-389-167
US-08-171-389-167
US-08-18-2-28A-157
US-08-18-2-28A-157
US-08-18-2-28A-167
US-08-18-2-28A-169
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US-08-450-673C-69
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  69, Appl
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159, App
159, App
159, App
170, App
167, App
167, App
167, App
169, App
                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 76 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
US-08-454-557C-69
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                                               Query Match
Best Local Similarity
Matches 58; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 69, Application US/08454557C Patent No. 5830670 GENERAL INFORMATION:
                                                                                                                                                                                           TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: (
  CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A. ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                  0.2%; Sc
llarity 100.0%; P
Conservative 0;
                                                    Score 58; DB; Pred. No. 2.1
0; Mismatches
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US-08-669-721-5	US-08-255-889-10	PCT-US95-17111A-91	US-08-450-673C-91	US-08-340-426D-91	US-08-454-557C-91	US-08-222-177A-163	US-08-669-721-5	PCT-US95-17111A-92	US-08-450-673C-92	US-08-340-426D-92	US-08-454-557C-92	PCT-US95-17111A-67	US-08-450-673C-67	US-08-340-426D-67	US-08-454-557C-67	US-08-859-998-318	PCT-US93-12388-169	US-08-482-080A-169
73	Sequence 10, Appl	Sequence 91, Appl			~				Sequence 92, Appl		•	•	•		Sequence 67, Appl		Sequence 169, App	

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APPLICATION UMBER: US/08/454,557C
APPLICATION: 30-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.384000:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Sterne, Kessler, Goldstein & Fox P.L.L.C
1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                           Release #1.0, Version
                                                            0609.3840003
                                                                                                                                                                                                                                                                   #1
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DB 3; Lc. 5. 2.1e-10; 0;

Length 76

Indels

0;

Gaps

0

RESULT 2 US-08-340-426D-69

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COUNTRY: U.S.A.

COUNTRY: U.S.A.

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPATED:

OPERATING SYSTEM: DC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/340,426D

FILING DATE: 14-NOV-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Ludwig, Steven R.

REGISTRATION NUMBER: 36,203

REGISTRATION NUMBER: 36,203

REFERENCE/DOCKET NUMBER: 0609.3840002

TELEFONDE: (202) 371-2600

TELEFAX: (202) 371-260

TELEFAX: (202) 371-2540

TON FOR SEQ ID NO: 69:

"TON FOR SEQ ID NO: 69:
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US-08-450-673C-69
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Best Local S
Matches 58
                                                                                                                                                                                                                                                                                                                                Sequence 69, Application US/08450673C Patent No. 5948888
                                                                                                                                                                                GENERAL INFORMATION:

APPLICANT: de la Monte, Suzanne
APPLICANT: wands, Jack R.

TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2685 GCCCCGCTAATTTTTGTATTTTTAGTAGAGAGAGAGGTTTCACCGTGTTGGCCAGGATG 2742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
ITILE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
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                                                                 COUNTRY: U.S.A. ZIP: 20005-3934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.0%; | es 58; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ce 69, Application US/08340426D No. 5948634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Sterne, Kessler, Goldstein & Fox P.L.L.C. 1100 New York Avenue, Suite 600
                                                                                                                                             E: Sterne, Kessler, Go
1100 New York Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             both
                                                                                                                                               Kessler, Goldstein & Fox P.L.L.C ork Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.2%; Score 58; DB 4; Length 76; 100.0%; Pred. No. 2.1e-10; Indels 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 76 base pairs
                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/3/
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R
                                                                                                                                                                  NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 06:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
       TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1100 New CITY: Washington STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
ZIP: 20005-3934
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                                                                                                                                                                                                                 , Steven K.
, Steven K.
36,203
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RECISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELECAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGGTH: 76 base pairs
                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 30-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,673C
. Match 0.2%; Score 58; DB 4; Local Similarity 100.0%; Pred. No. 2.1e-10; les 58; Conservative 0; Mismatches 0;
                                                                                                                                      nucleic acid
DEDNESS: both
                                                                                                                                                                                                                                                                                                   0609.3840004
                                       Length 76;
  Indels
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Gaps

Sequence 69, Application PC/TUS9517111A GENERAL INFORMATION: COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PG PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATION NUMBER: PC-DOS/MS-DOS
APPLICATION NUMBER: PC-DOS/MS-DO CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 08/340,426 TITILE OF INVENTION: Neural Thread Protein Gene Expression and TITLE OF INVENTION: Detection of Alzheimer's Disease NUMBER OF SEQUENCES: 121 APPLICANT: de la Monte, Suzanne APPLICANT: Wands, Jack R. CORRESPONDENCE ADDRESS E: Sterne, Kessler, Goldstein & Fox P.L.L.C 1100 New York Avenue, Suite 600 Release #1.0, Version #1.25 PCT/US95/17111A

0609.3840002

ADDRESSEE:

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                                                                                                                                   RESULT 6
US-08-340-426D-57
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                                                        Sequence 57, Application US/08340426D Patent No. 5948634
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne APPLICANT: Wands, Jack R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 58; Conserv
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                                                                                                                                                                                                                                                                                           Query Match
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: de la Monte, S
APPLICANT: Wands, Jack R.
                         TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: bo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/454,557C FILING DATE: 30-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                        TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
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20005-3934
                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
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                                                                                                                                                                                                                                                              Conservative
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Pred. No. 2.1e-10;
                                                                                                                                                                                                                                                                            Score 55;
Pred. No.
                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                            DB 3;
. 2e-09;
                                                                                                                                                                                                                                                                                           Length 60;
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description US/08450673C Patent No. 5948888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/340
FILING DATE: 14-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwidy, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELECOMMUNICATION TOTAL
             CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (202) 371-25
INFORMATION FOR SEQ ID NO:
                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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LENGTH: 60 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: de la Monte,
APPLICANT: Wands, Jack
                                                                                                                             APPLICATION NUMBER: US/08/450,673C
FILING DATE: 30-MAY-1995
                                                                                                                                                                                                                                                                                                                                        STREET: 1100 New CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 60 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1100 New CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A. ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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20005-3934
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                                                                                                                                                                                                                                                                                                                                                              3: Sterne, Kessler, Goldstein & Fox P.L.L.C
1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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202)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0609.3840002
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5. 2e-09;
0;
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TOPOLOGY:
US-08-450-673C-57
RESULT 9
US-08-171-389-159/c
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                                                                                                                                                                                                                                                                                                                                              TELEFAX: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 base no'--
Type:
                                                                                                                                                                       Query Match
Best Local Similarity
Matches 55; Conserv
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O.2%; Score 55; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 2e-09;
Matches 55; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2685 GCCCGCTAATTTTGTATTTTAGTAGACAAGGGTTTCACCGTGTTGGCCAGG 2739
                                                                                   APPLICANT: de la Monte, Jack R.
APPLICANT: Wands, Jack R.
APPLICANT: Disease
TITLE OF INVENTION: Detection of Alzheimer's Disease
TITLE OF SEOUENCES: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FORM:
COMPUTER: PSYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/34
FILING DATE: 14.NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 60 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1100 New CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                      LENGTH: 60 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Sterne, Kessler, Goldstein & Fox P.L.L.C. 1100 New York Avenue, Suite 600
                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                       both
                                                                                                                                                                         0.2%; Score 55; DB 6; Length 60
100.0%; Pred. No. 2e-09;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                         Indels
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                                                               RESULT 10
US-08-123-936-159/c
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; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: Human H4/a gene for US-08-171-389-159
APPLICANT: LULIN, LISA M.

APPLICANT: LULIN, LISA M.

TITLE OF INVENTION: Sequence-Directed DNA Binding
TITLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 641
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 159, Application US/08171389 Patent No. 5578444
                                                                                  Query Match
Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION NUMBER: US 08/081,070
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
ANAME: FENTAN GATVE
                                                                                                                                                                                                                                                                                                       TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 159:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/171,389
                                                                                                                                                                                                                                             MOLECULE TYPE: UN
                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 46
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Fabian, Gary
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94063
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                                                                               0.2%; Score 48; DB 1; ilarity 100.0%; Pred. No. 4.1e-07 Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Edwards, Cynthia Cantor, Charles
                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                  DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gary R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cynthia A. Charles R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33,875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4600-0175/G19P3
                                                                                                                                                                                                            H4 histone
                                                                                                                       Length 48;
                                                                                    Indels
                                                                                  0;
                                                                                    Gaps
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Sequence 159, Application US/08123936 Patent No. 5726014 GENERAL INFORMATION:

0;

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; MOLECULE TYPE: DNA (9; HYPOTHETICAL: NO ORIGINAL SOURCE: INDIVIDUAL ISOLATE: US-08-123-936-159
                                                                                                                                                                                                       RESULT 11
US-08-475-228A-159/c
                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                         Sequence
                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (415) 324-086
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/723,618
APPLICATION NUMBER: 27-JUN 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                      22582 GAGAGAATAGGAAACCGATCTTTATATATCTACGTTACCCCTGCCCCC 22629
                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                               APPLICANT: Fry, Kirk E. TITLE OF INVENTION: Seq. TITLE OF INVENTION: Mol. NUMBER OF SEQUENCES: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Screening Assay for the Detection of TITLE OF INVENTION: DNA-Binding Molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (415) 324-0880
              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                     48
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FILING DATE:
                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 505 Penobscot Drive CITY: Redwood City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Fablan, Gary R. REGISTRATION NUMBER: 33,875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH:
                                                                                                                                                                                                                                                                   GAGAGAATAGGAAACCGATCTTTATATATCTACGTTACCCCTGCCCCC 1
                                                                                                                                                                      59, Application US/08475228A
5869241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
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                                                                                                                         Edwards, Cynthia A
Cantor, Charles R.
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                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                            Andrews, Beth M.
Turin, Lisa M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Genelabs Technologies, Inc
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                                Molecules, Compositions and Methods 664
                                                                                                                                                                                                                                                                                                                                                 0.2%;
                                                           Sequence-Directed DNA Binding
                                                                                                                                          Cynthia A
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US-08-475-228A-159
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US-08-482-080A-159/c
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                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                      APPLICANT: Turin
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                                                            ADDRESSEE:
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Sequence 159, Application US/08482080A Patent No. 6010849
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                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/723,618
FILING DATE: 27-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/081,070
FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/475,2284
FILING DATE: 06-JUN-1995
PRIOR APPLICATION UNMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                     APPLICANT: Edwards, Cynthia A
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                     TITLE OF INVENTION: Sequence-Directed DNA Binding TITLE OF INVENTION: Molecules, Compositions and Methods NUMBER OF SEQUENCES: 664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 23-DEC-1992 PRIOR APPLICATION DATA:
                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 503.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 4600-0175.21/G19P3D2
                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Stratford, Carol A. REGISTRATION NUMBER: 34,4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
Redwood City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
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                E: Genelabs Technologies, Inc
505 Penobscot Drive
                                                                                                                                            Turin,
                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                            Edwards, Cynthia A.
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                                                                                                                       n, Lisa M.
Kirk E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   double
                                                                                                                                                                                                                                                                                                                                                                                                                               0.2%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                 4.1e-07
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PCT-US93-12388-159/c

; Sequence 159, Application PC/TUS9312388

; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMEDIUM TIKE: FLOPPY ULDA

COMEDIER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Vers

SOFTWARE: Patentin Release #2.0, Vers

APPLICATION NUMBER: US/08/482,080A

FILING DATE: 07-JUN-1995

PRIOR APPLICATION NUMBER: US 08/171,389

FILING DATE: 07-DEC-1993

PRIOR APPLICATION NUMBER: US 08/123,936

FILING DATE: 17-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/996,783

FILING DATE: 23-DEC-1992

PRIOR APPLICATION NUMBER: US 07/723,618

FILING DATE: 27-JUN-1991

APPLICATION NUMBER: US 07/723,618

FILING DATE: 27-JUN-1991

PRIOR APPLICATION NUMBER: US 08/081,070

FILING DATE: 27-JUN-1993

ATTORNET/AGETI INFORMATION:

REGISTRATION NUMBER: 39.118

REFERENCE/DOCKET NUMBER: 39.118

REFERENCE/DOCKET NUMBER: 39.118

REFERENCE/DOCKET NUMBER: 39.118

REFERENCE/DOCKET NUMBER: 39.118

TELEPHONE: (650) 324-0860

INFORMATION FOR SEQ ID NO: 159:

SEQUENCE CHARACTERISTICS:

LENGTH: 48 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.2%; Score 48; DB 5; Best Local Similarity 100.0%; Pred. No. 4.1e-07 Matches 48; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22582 GAGAGAATAGGAAACCGATCTTTATATATCTACGTTACCCCCGCCCCC 22629
                                                                                                                                                  TITLE OF INVENTION: Sequence-Directed DNA Binding TITLE OF INVENTION: Molecules, Compositions and Methods NUMBER OF SEQUENCES: 641
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genelabs Technologies, Inc.
STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: UN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: UZIP: 94063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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                                                                                                                                     USA
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NAME: Fabian, Gary R.

REGISTRATION NUMBER: 4600-0175.41/G19PCT2

REFERENCE/DOCKET NUMBER: 4600-0175.41/G19PCT2

TELECOMMUNICATION INFORMATION:

TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 159:

SEQUENCE CHARACTERISTICS:

LENGTH: 48 base pairs

TYPE: nucleic acid

TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
PCT-US93-12388-159
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US-08-171-389-170
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                                                                                                                                                                                                                                                                                                            APPLICANT: Turin, Lisa M.

APPLICANT: Fry, Kirk E.

APPLICANT: Fry, Kirk E.

TIFLE OF INVENTION: Sequence-Directed DNA Binding
TIFLE OF INVENTION: Molecules, Compositions and Methods
NUMBER OF SEQUENCES: 641

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genelabs Technologies, Inc.

STREET: 505 Penobscot Drive
CITY: Redwood City
STATE: CA
COUNTRY: USA
COUNTRY: USA
21P: 94063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 55/0...
Patent No. 55/0...
Patent INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 170, Application US/08171389 Patent No. 5578444
APPLICATION NUMBER: US/08/171,389
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/123,936
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
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PRIOR APPLICATION UNBER: US 08/
PILING DATE: 17-SEP-1993
PRIOR APPLICATION UNBER: US 07/
APPLICATION UNBER: US 07/
FILING DATE: 23-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                              ZIP: 94063
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Edwards, Cynthia A
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL: I
ORIGINAL SOURCE
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APPLICATION NUMBER: PCT/US93/12388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MBER: US 07/996,783
23-DEC-1992
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Gaps

FILING DATE: 23-DEC-1992 PRIOR APPLICATION DATA:

US 07/723,618

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US-08-123-936-170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; INDIVIDUAL ISOLATE: US-08-171-389-170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 0.2%;
Best Local Similarity 100.0%;
Matches 47; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 170, Application US/08123936 Patent No. 5726014 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12078 CAATAGTTGGTGGTCTGACTCTATAAAAGAAGAGTAGCTCTTTCCTT 12124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 47 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415) 324-0960 INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 22-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: FADIAN, GATY R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 4600-0175/G19P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DN
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                APPLICATION NUMBER: US 07/723,618 FILING DATE: 27-JUN-1991 ATTORNEY/AGENT INFORMATION:
                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/996,783
FILING DATE: 23-DEC-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Edwards, Cynthia A.
APPLICANT: Cantor, Charles R.
APPLICANT: Andrews, Beth M.
APPLICANT: Turin, Lisa M.
TITLE OF INVENTION: Screening Assay for the Detection
TITLE OF INVENTION: DNA-Binding Molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 0: FILING DATE: 27-JUN-1991 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 0:
                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Genelabs Technologies, Inc. STREET: 505 Penobscot Drive CITY: Redwood City
                                                                                                                                                                                                                                                                                                                                                            COUNTRY: UZIP: 94063
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CAATAGTTGGTGGTCTGACTCTATAAAAGAAGAGTAGCTCTTTCCTT 47
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8.8e-07;
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                                                     Query Match
Best Local Similarity
Matches 47; Conserv
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEPAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 170:
MOLECULE TYPE: DN
HYPOTHETICAL: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 47 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                       STRANDEDNESS: double
                                                                                                                                                                                                TOPOLOGY:
                                                        Conservative
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                                                                   0.2%; Score 47; DB 2; I
100.0%; Pred. No. 8.8e-07;
                                                                                                                                          Human histone H3 gene
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                                                       0
                                                        Mismatches
                                                                                Length 47;
                                                        Indels
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Search completed: March 30, 2000, 17:28:35 Job time: 135577 sec

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Page 8

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Minimum DB seq length: 8
Maximum DB seq length: 105
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Perfect score:
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13816.393 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

c 1	Result
53	sult Query No. Score Match Length DB ID
0.2	Query Match
98	Length I
31	₩
c 1 53 0.2 98 31 AA280198 AA280198 zt04b12.	ID
AA280198 zt04b12.r	Description

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JOURNAL COMMENT
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N zt04b12.rl NCI_CGAP_GCB

similar to contains Alu

repetitive element ;, mi

AA280198.1 GI:1921755

EST.
National Law.
Tumor Gene Index
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced y....
On Sep 12, 1996 this sequence version replaced y....
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 98)
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National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                  98 bp mRNA EST 11-AUG-1997 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712127 5' contains Alu repetitive element;contains element MER22 element; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                AI864984
AA8098185
AA80983186
AI591270
AQ535244
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AA578614
AA57861
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AA129957

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AA5551166

AA649287

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ZA916300

AI708433

H67549

AA235077

AA8352057
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                                                                                                                                                                                                                                                                                                                                                                                                          AI864984 wk06c11 x
AA80981 co40f11 x
AA57816 xpc1-11-3
AA53524 xpc1-11-3
AA53524 xpc1-11-4
AI832832 at7299 x
AA614379 np46c03 x
AA614379 np66c03 x
AA614379 np66c11 co4012 cox
AA628110 co4012 cox
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AA645287 ra66d10 x
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AA614587 ra66d04 x
AA61565 ra66d04 x
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AA61577 ra66d04 x
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AQ319270 ReC111-98
F29274 HSPD19063 H
AA457423 aa86b02.r
A1932967 wc40f09.x
AQ626158 CITB1-E1-
D25879 HUMGS05672
B48914 RPC111-4A12
A1864984 wx06c11.x
A1801185 tc79h04.x
AR809831 ca40f11.s
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yc05f08.r1 S
IMAGE:79815
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53; Conserv
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T64089
T64089.1 GI:667954
EST.
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The vector to vector length is 99
Insert Length: 622 Std Error: 0.00
Seq primer: -28m13 rev2 ET from Amersham.
Location/Qualifiers
                                                                                                                                                                              Genome Res.
97044478
                                                                                                                                                                 Contact: Wilson RK
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larity 100.0%;
Conservative
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2568 CCCAGGCTGGAGTGCAATGGCGCGATCTCGGCTCACTGCAACCTCCGCTTCCC
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1 (bases 1 to 70)

1 (bases 1 to 70)

1 (chisse, L. Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chisses, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Mardis, E., Schellenberg, K., Soares, M.B., Tan, F., Thierry, Meg, J., Travaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R., and Marra, M.
High qality sequence stops: 54
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: M13RP1
                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. I Tel: 314 286 1800 Fax: 314 286 1810 F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
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//Clone_Llb="NGI_CGAP_GCB1"
//Llsue_type="germinal center B cell"
//Llb_host="DHIOB"
//Lb_host="DHIOB"
//Lb_host="DH
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                            Email: hbe@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu/. Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genetics (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1998)
Other_GSSs: RPCI11-98B22.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 102)
Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
Berry,K., Granger,D., Suh.E., Wible,C., de Jong,P. and Venter,J.C.
Use of human BAC End Sequences for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genomic survey sequence.
AQ319270
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eq primer: SP6
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Location/Qualifiers
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/db_xref="GDB:7537293"
/db_xref="taxon:9606"
/clone="RPCI-11-98B22"
                                                                /sex="Male"
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'note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
                                                                                    clone_lib="RPCI-11"
                                        cell_type="Lymphocytes"
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100.0%;
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hes 0;
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24 GGCGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAA
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                                                                          43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ευκαιγοτα; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 91)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       University of Pad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRIBI Biotechnology Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Valle G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Apr 7, 1998 this sequence version replaced gi:3034419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSPD19063 HM3 Homo sapiens cDNA clone s4000074G04, mRNA sequence.
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                                                                                                                                                                                      18
                                                                        Conservative
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                                                                                                                                                                                    ds cDNA was sonicated and size-selected in the range 350-550 bp. The 3' specific fragments were selected by streptavidin coated magnetic beats, ligated to non-palindromic BstXI adapters, NotI digested and directionally cloned into BstXI-NotI cut pcDNAII vector." a 19 c 38 g 16 t
                                                                                                                                                                                                                                                                                             /Tissue_type="pectoral muscle (after mastectomy)"
/note="Vector: pcDNAII (Invitrogen); Site_1: BstXI;
Site_2: NotI; The library was constructed by G.
Lanfranchi. This library is not subtracted nor normalized.
The first strand cDNA was primed with a blottinylated
oligo-dT-NotI primer
(5'-blotin-AACCCGGCTTCAGCGGCCGCCTTTTTTTTTTTTTTTTT-3'). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="s4000074G04"
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es 42; Conserv
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                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 92)
11 (bases 1 to 92)
12 (CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
                                                                                                                                                                                                                                                                                                               AI932967 92 bp mRNA EST 02-SEP-1999 w040f09.xl NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2457833 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: 28ml3 rev1 ET from Amersham High quality sequence stop: 76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, Tel: 314 286 1800
Fax: 314 286 1810
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1 (bases 1 to 95)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost, Rucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylle,T., Waterston,R. and Wilson,R.

WashU-Merck EST Project 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
On Nov 4, 1996 this
Contact: Wilson RK
Unpublished (1997)
On Dec 20, 1995 this sequence version replaced gi:1134104.
                                                                                                                                                                                                                                                 AI932967
AI932967.1 GI:5671704
                                                                                                                                                                                                                                                                                             mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
This clone is available roya
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//note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
//note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dT. Pooled
retinal tissue. Average insert size: I.O kb; Uni-ZAP XR
Vector: -5' adaptor sequence: 5' GRATICGGCACGAG 3' -3'
vector: -5' adaptor sequence: 5' CTCCAGTTTTTTTTTTTTTTTTTT 3'"

adaptor sequence: 5' CTCCAGTTTTTTTTTTTTTTTTTT 3'"

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/db_xref="taxon:9606"
/clone="IMAGE:838155"
/clone_lib="Stratagene fetal retina 937202"
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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AQ626158/c
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                                                                                                                                                                                                                                                                        Unpublished (1997)
Other_GSS8: CITBI-21-2650p18.TF
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQ626158.1 GI:5088550
GSS.
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CITBI-E1-2650P18.TR CITBI-E1
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Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
Emmert-Buck, M.D., Ph.D.
                                                                     end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 104)
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                                                                                                                                                                                                     9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genomic survey sequence.
                                                                                                                                                          Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
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                                                                                                                                                                                                                                                                                                                                                                                                         Use of BAC End Sequences from CalTech Libraries for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"Organ: Stomach; Vector: pCMV-SPORT6; Site_1: Sal
Site_2: NotI; Cloned unidirectionally. Primer: Oligo of
Average insert size 1.69 kb. Life Technologies catalog
11549-011"
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/db_xref="taxon:9666"
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/tissue_type="poorly differentiated adenocarcinoma with
signet ring cell features"
/lab_host-"DH10B"
       /organism="Homo sapiens"
                                                Location/Qualifiers
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clone 2650P18,
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nes 41; Conservative (
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1 (bases 1 to 52)

Okubo, K., Yoshii, J., Yokouchi, H., Kameyama, M. and Matsubara, K. Global analysis of gene expression in colon mucosa: a large scale random cDNA sequencing analysis

Unpublished (1994)

Contact: Okubo, K., Itoh, K., Yoshii, J., Yokouchi, H. and Matsubara, K Institute for Molecular and Cellular Biology

Osaka University

Osaka University

J Yamada-oka, Suita, Osaka 565, Japan.
                                                           GSS.
                                                                                                 B48914 103 bp DNA RPCII1-4A12.TP RPCI-11 Homo genomic survey sequence.
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EST.
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D25879
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                                                                      B48914.1 GI:2601151
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                          Homo sapiens
                                                                                                                                                                                                                                                                       0.1%; Score 40; DB 20; llarity 100.0%; Pred. No. 0.0031; Conservative 0; Mismatches 0
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                                                                                                                                                                                                                                                                                                                                                       /clone="cm2335"
/clone_lib="Human colon mucosa"
/note="Adult male, tissue_type =
17 c 14 g 9 t
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/note="Vector: pBeloBAC11; Site_1: EcoR1;
CalTech Human BAC Library D"
28 c 22 g 42 t
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/db_xref="taxon:9606"
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/clone_lib="CITBI-E1"
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clone RPCI-11-4A12,
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similar to
                     Unpublished (1997)
On May 18, 1998 this sequence version replaced gi:3137794.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Life Technologies catalog #: 11547-015
DNA Sequencing by: Washington University Genome Sequencin
Clone distribution: NCI-CGAP clone distribution informati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40;
                                                                                                                                                                                                                                               Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 90)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu/ordering) or from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (lifo@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
Contact: Wark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venter, J.C.
Use of BAC End Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 103)
Adams,M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P.
                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A1864984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AI864984
                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                      AI864984.1 GI:5529091
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                                                                                                                                                                                                                               Tumor Gene Index
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  primer: SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.1%; Score 40; DB 81; llarity 100.0%; Pred. No. 0.0022; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cell_type="Lymphocytes" Site_1: EcoRI; Site_2: EcoRI; note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; RPCIII Human Male BAC Library" 28 c 30 g 15 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1. .103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="GDB:7501163"
/db_xref="taxon:9606"
/clone="RPCI-11-4A12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90 bp mRNA EST 30-AUG-1999 NCI_CGAP_Lyml2 Homo sapiens cDNA clone IMAGE:2411540 3' contains Alu repetitive element; mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 103;
                                              Sequencing (
                                                                                                                                                                                                                                                    Project (CGAP),
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                                              n can be
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primer:

-40UP from Gibco

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REFERENCE
AUTHORS
TITLE
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AI801185/c
LOCUS
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VERSION
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Best Local S
Matches 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: Robert_Strausbergenih gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[ [bases 1 to 35]
                                                                                                                                                                                                                                                                                                                                                                                                     Seg primer: -400P from Gibco High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1997)
On Mar 16, 1998 this sequence version replaced gi:2961671
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA sequence.
AI801185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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37; Conservative
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a 29 c 27 g 21 t
/note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. primer: Oligo dT. Average insert size 1.69 kb. Life Technologies catalog #: 11549-011"
                                                                                                                    /Clone="IMAGE:2184535"
/Clone_lib="NOI_CGAP_Gas4"
/tissue_type="poorly differentiated adenocarcinoma with
/tissue_tring cell features"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9606"
/clone='InAGE:2411540"
/clone_lib="MCI_CGAP_Lym12"
/fisue_type="lymphoma, follicular mixed small and large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No.
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0.025;
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AUTHORS
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VERSION
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AA809831/c
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ORIGIN
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ORGANISM
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Query Match
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wes 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: Robert_Strausberg@nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., D
Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.,
Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1997)
On Jan 19, 1998 this sequence version replaced g1:2287025.
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insert Length: 963 Std Error: 0.00 Seg primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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National Cancer Institute, Cancer Genome Anat
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases.1 to 88)
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AA809831
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                                                                                                                                                                                                                                                                                                                                         /note-"vector: pT/T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Ecc Ri; Ist strand create prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+ IgD-), provided by Dr. Louis M. Staudt (NCI), Dr. David Allman (NCI) and Dr. Gerald Marti (CBER). cDNA synthesis was primed with a Not I - oligo(dT) primer
                                                                                                                        /tissue_type="germinal center B cell"
/tab_host="belos"
/note="vorte="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:1307469"
/clone_lib="NCI_CGAP_G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No.
   Score
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   35;
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   38;
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   Length 88;
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ibution information can b
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source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer: Promote Stop: 65. High quality sequence stop: 65. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1093
High quality sequence stops: 65
Source: IMAGE Consortium, LINL-free through LINL; contact the
This clone available.
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1093 Std Error: 0.00
Seq primer: Promega -21m13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 96)
Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R67088 96 bp mRNA EST 30-MAY y130h05.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:140793 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On Apr 5, 1995 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
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Eutheria; Primates; Catarrhini; Hominidae; Homo
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Conservative 0;
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                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="GDB:549405"
/db_xref="taxon:9606"
/clone="IMAGE:140793"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib-"Soares placenta Nb2HP"
                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="Female"
                                                                                             100.0%;
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                                                                                                                                                                                                                                    44 GTGAAACCCCGTCTCTACTAAAAAAAAAAAAAAAA 78
                                    AQ535244 103 bp DNA GSS 18-RPCI-11-317H22.TV RPCI-11 Homo sapiens genomic clone RPCI-11-317H22, genomic survey sequence.
AQ535244
AQ535244 GI:4846934
GSS.
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35; Conserv
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Unpublished (1997)

On Mar 20, 1998 this sequence version replaced gi:2980211.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AI591270 102 bp mRNA EST 21-APR-1999 tt76a04.x1 NCI_CGAP_HSC3 Homo sapiens cDNA clone IMAGE:2246670 3 similar to contains Alu repetitive element; contains element MER4 repetitive element; , mRNA sequence.

AI591270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: -40UP from Gibco.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Preparation: David B. Krizman, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 102)
  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    51
                                                                                                                                                                                                                                                                                                                                                                                                                            /note-*Organ: bone marrow; Vector: pAMP1; mRNA made from lymphoid tissue, cDNA made by oilgo-dr priming. Directionally cloned. Size-selected on agarose gel, average insert size 500 bp. Primary library, non-amplified. cDNA Library Preparation: David B. Krizman, Ph.D. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:2246670"
/clone_lib="NCI_CGAP_HSC3"
/tissue_type="CD34+, T negative, patient with chronic myelogenous leukemia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                0.1%; Score 35; DB 48; Length 102; 100.0%; Pred. No. 0.12;
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                                                                                                  63 CCAGGCTGGTCTCGAACTCCTGACCTCAAGTGATC 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: hbe@tigr.org

Clones are derived from the human BAC library RPCI-11. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genet os (lifo@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.

Seg primer: T7

Class: BAC ends.
                                                                                                                                                                                                                                                                                              31
                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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/clone="taxon:9606"
/cell_type="Lymphocytes"
/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
a 27 c 27 g 18 t
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OLIGO_NUC , Gapop 60.0 ,

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X74432 H. sapiens (
X03556 Human low d
X57789 Human seque
A68621 Sequence 1
L30829 Human STS U
L36843 Homo sapien
L29838 Human STS U
L30919 Human STS U
A08915 H. sapiens (
M36133 Human albha
M30167 D. melanogas
M31539 D.melanogas
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L36843 Homo sapien
D17279 Human Hep62
U24138 Hylobates s
AF087511 Homo sapi
S73203 ALL-1 (tand
M36131 Human alpha
AF08459 Homo sapi
AF08459 Homo sapi
AF08459 Homo sapi
AF08459 Homan fari
M4189 Human flow d
M14179 Human flow d
M14179 Human alpha
AF032238 Otolemur
M14180 Human low d
M14179 Human alpha
M36131 Human alpha
M36131 Human alpha
M36132 Human alpha
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HUMALUANCD
LOCUS
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Db 16 TTTTTGTATTTTAGTAGAGACAGGGTTTCACCGTGTT 53
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Best Local Similarity 100.0%; Pred. No. 2.2e-07
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                                                                                                                                                                  Homo sapiens 4000 year old r
fragment 12:5.
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1 (bases 1 to 76)

1 (bases, S. and Wands, J.R.

Neural thread protein gene expression and detection of Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AR051499 76 bp DNA
Sequence 69 from patent US 5830670.
AR051499
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1 (bases 1 to 60)

1 (bases 1, 5, and Wands, J.R.

Neural thread protein gene expression and detection of Alzheimer's disease
Ancient DNA: extraction, characterization, molecular cloning, and enzymatic amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent: US 5830670-A 69 03-NOV-1998; Location/Qualifiers
                                                                                        Homo sapiens
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                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                      Homo sapiens (individual_isolate 4000 year old remains from
Nekht-ankh) liver DNA.
                                                                                                                                      Alu repeat.
                                                                                                                                                  L36843.1 GI:556196
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remains from Nekht-ankh Alu repeat
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HUMD6B03M3/c
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                                                                                                                                                                                                                                                                                                                                                   Soraku-gun, Kyoto
Japan, 619-02
Phone: 07747-5-2308
Fax: 07747-5-2321
ch 0.1%; Score 35; DB 9; 1 Similarity 100.0%; Pred. No. 6.8e-06. 35; Conservative 0; Mismatches 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (21-JUL-1993) to the DDBJ/EMBL/GenBank databases. Ryo
Submitted (28-JUL-1993) to the DDBJ/EMBL/GenBank databases. Ryo
Matoba, Osaka University, Institute for Molecular and Cellular Bio;
1-3, Yamada-oka, Suita, Osaka 565, Japan
(E-mail:matoba@inherit.imcb.osaka-u.ac.jp,
Tel:81-6-877-511(ex.3314), Fax:81-6-877-1922)
2 (bases 1 to 51)
Matoba, R., Okubo, K., Hori, N., Fukushima, A. and Matsubara, K.
The addition of 5'-coding information to a 3'-directed cDNA library
Amproves analysis of gene expression
Gene 146 (2), 199-207 (1994)
94357437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 0.1%; Score 36; DB 9; I Similarity 100.0%; Pred. No. 2.1e-06; 36; Conservative 0; Mismatches 0;
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89184542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene signature.
Homo sapiens Male cell_line:HepG2 cDNA to mRNA, clone_lib:Kiseru.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMD6B03M3 51 bp mRNA PRI Human HepG2 3' region MboI cDNA, clone hmd6b03m3.
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D17279.1 GI:598922
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Molecular Microbiology and Genetics Lab.
Research Institute of Innovative Technology for the Earth 9-2
Kizugawadai Kizu-cyo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (21-Jul-1993) to DDBJ by:
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Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Hep62"
/clone_lib="Kiseru"
/sex="Male" 12 g 7
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18 c 23 g
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/isolate="4000 year old remains from Nekht-ankh"
/db_xref="taxon:9606"
/tissue_type="liver"
<1. >67
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.

1 (bases 1 to 79)

Arcot,S.S., Wang,Z., Weber,J.L., Deininger,P.L. and Batzer,M.A.

Alu repeats: a source for the genesis of primate microsatellites

Genomics 29 (1), 136-144 (1995)
                                                                                                                                                                            AF087511 66 bp mRNA
Homo sapiens clone ENaC+22 epithelial
(SCNNIA) mRNA, alternatively spliced,
AF087511
AF087511.1 GI:5870626
                                                                                                                                                                                                                                                                                                                                                                                        0.1%; Standarity 100.0%; 35; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (30 MAR-1995) James L. Weber, Medical Genetics,
Marshfield Medical Research Foundation, 1000 N. Oak Ave.,
Marshfield, WI 54449, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dispersion and insertion polymorphism in recently amplified human Alu repeats J. Mol. Biol. 247 (3), 418-427 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 79)
Batzery, A. Pubin, C.M., Hellmann-Blumberg, U., Alegria-Hartman, M.,
Leeflang, E.P., Stern, J.D., Bazan, H.A., Shaikh, T.H., Deininger, P.L.
and Schmid, C.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hylobates sp. sequence homologous to Human dinucleotide repeat region clone Mfdl58, sequence tagged site.
                              An Alu cassette in the human Unpublished
                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 65)
Oh,Y. and Warnock,D.G.
                                                                                                                             Homo sapiens
                                                                                                                                               human.
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   Oh, Y.
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(bases 1 to 66)
Y. and Warnock, D.G
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/db_xref="taxon:9581"
/chromosome="7"
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. 6.7e-06;
thes 0;
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Submitted (26-AUG-1998) Medicine,
Birmingham, AL 35294, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenBank staff at the National Library of Medicine created entry [NCBI gibbsq 155288] from the original journal artic This sequence comes from Fig. 3a.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Mammalia; M
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                                                                                                          33; Conserv
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ALL-1 tandem duplication in acute myeloid leukemia with a normal karyotype involves homologous recombination between Alu elements Cancer Res. 54 (16), 4277-4280 (1994)
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/note="alternatively spliced epithelial sodium channel alpha subunit containing intronic Alu sequence"
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/db_xref="taxon:9606"
/chromosome="12"
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/db_xref="taxon:9606"
1. .79
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DEFINITION Homo sapiens core-binding 5, partial sequence.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 80)
1 (bases 1, bishop,D.F. and Desnick,R.J.
Kornreich,R., Bishop,D.F. and Desnick,R.J.
Alpha-galactosidase A gene rearrangements causing Fabry disease.
Identification of short direct repeats at breakpoints in an
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Human alpha-galactosidase breakpoint family F.
M36132
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1 (Dases 1 to 80)

2 (Dases 1 to 8
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Human alpha-galactosidase breakpoint region.
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/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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Local Similarity 100.0%; Pred. No. 0.00066;
Nes 31; Conservative 0; Mismatches 0; Indels
                                                  2 (bases 1 to 76)
2 (bases 1 to 76)
2ietklewicz,E., Richer,C., Sinnett,D. and Labuda,D.
Direct Submission
Submitted (31-CGT-1997) Pediatry, University of Montreal,
Submitted (31-CGT-1997) Pediatry, University of Montreal,
Sainte-Justine Hospital, Research Center (Charles Bruneau Center of
Cancerology), 3175 Cote Sainte-Catherine, Montreal, Quebec H3T-1C5,
                                                                                                                                                                                                                                           thick-tailed bush baby.
Otolemur crassicaudatus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Strepsirhini; Galagonidae; Otolemur.
1 (bases 1 to 76)
2 ietkiewicz, E., Richer, C., Sinnett, D. and Labuda, D.
Monophyletic origin of Alu elements in primates
J. Mol. Evol. 47 (2), 172-182 (1998)
   Canada Sequences corresponding to the PCR primers used to amplify
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Otolemur crassicaudatus
AF032238
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Direct Submission
Submitted (20-AUG-1998) Hematology, Erasmus University Rotterdam, Dr. Molewaterplein 50, Rotterdam 3015 GE, The Netherlands
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF032238.1 GI:2642069
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Jagmohan-Changur,S. and Breuning,M.H.
Nonoverlapping genomic inv(16)(p13q22) CBFB intron 5 breakpoint
regions ordered centromeric to telomeric
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 60)
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AF084969.1 GI:3659831
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/db_xref="taxon:9606"
/chromosome="16"
/map="16922"
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          ch 0.1%; Solid Similarity 100.0%; I 31; Conservative 0;
                                                                          /note="deletion target sequence"
19 a 34 c 25 g 19 t
Chromosome 19p13.2-p13.1.
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J. Biol. Chem. 261 (28), 13114-13120 (1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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low density lipoprotein receptor
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/clone="GALII27"
                                                                                                                                             /gene-"LDLR"
/note-"LDLR intron
                                                                                                                                                                                                     /map="19p13.3"
join(M14178_1:1. .97,1.
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20 c 21 g
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/db_xref="taxon:9606"
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           score 31; DB; Pred. No. 0.0
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gene (LDLR), intron 5
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Alu repeat.
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           /tissue_type="carcinoma"
27 c 33 g 1
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22242 CCTGTAATCCCAGCACTTTGGGAGGCCAAGG 22272
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1 (bases 1 to 103)

Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.
Alu RNA transcripts in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences
J. Mol. Biol. (1992) In press
J. Mol. Biol. (1992) The press
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HUMALCE221 103 bp ss-RNA PRI 15-APR-1994
Human carcinoma cell-derived Alu RNA transcript, clone CE221.
M87896
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J. Biol. Chem. 261, 13114-13120 (1986)
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1 (bases 1 to 97)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        low density lipoprotein receptor-1; very low density lipoprotein Human fibroblast DNA, from patient FH-626.
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/db_xref="taxon:9606"
42. 72
/dev_stage="embryo"
/sex="male"
                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="NTera2D1"
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Db 12 GCCCACCTTGGCCTCCCAAAGTGCTGGGAT 41
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80 bp DNA

Human alpha-galactosidase breakpoint region.

M36131

M36131. GI:179541

Fabry disease; breakpoint junction; glycosphingolipid catabolism.

Human DNA.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eukheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 80)

Kornreich, R., Bishop, D.F. and Desnick, R.J.

Alpha-galactosidase A gene rearrangements causing Fabry disease:
Identification of short direct repeats at breakpoints in an

All-rich gene
                                                                                                                                                                                                                                                                                                                                                                                                   Alu-rich gene
J. Biol. Chem. 265, 9319-9326 (1990)
90264427
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/db_xref="taxon:9606"
19 a 28 c 20 g 13 t
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length: 105
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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V70704
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                                                               Primer SINXball700
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Reverse
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PCR primer AL1. Nu
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    fragment
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ALIGNMENTS

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RESULT 1
Q55168/c
TD Q55168 standard; DNA;
s Synthetic.

y 307242700-A.

y 19-SEP-1995.

p 04-MAR-1994; 059906.

y 04-MAR-1994; 05906.

y 04-MAR-1994; 0590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 28
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D 06-JAN-1993; U06162.

P 23-JUN-1993; U05903421.

R 24-JUN-1992; US-903421.

A (CORR) CORNELL RES FOUND INC.

A (UNNY) UNIV NEW YORK MT SINAI.

SCHOOL MEDICINE.

Gelman IH, Laurence JC;

WPI; 94-026200/03.

HIV-LP useful in vaccine formulations - is novel HIV virus distinct from HIV-1 and or HIV-2 viruses

T distinct from HIV-1 and or HIV-2 viruses

Example; page 7; 75pp; English.

C HIV-LP is a new variant of the HIV family. A cDNA first strand was synthesised from Pt. 1 pellet using MLV RT. The product was converted into dsDNA and this cDNA was amplified by PCR using primers Q55167 and Q55168.

C primers Q55167 and Q55168.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29696 AAAAAAAAAAAAAAAAAAAAAAAAGAAT 29723
                                                                                                                                                                                                                                                                                                                                                                                                                                               Trypsin inhibitory protein cDNA antisense primer-1.
Trypsin; inhibitor; human T98G cells; pancreatitis; shock; DIC; multiple organ failure; disseminated intravascular coagulation;
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Sequence of primer for PCR amplification of HIV-LP Pt.1 isolate
Human immunodeficiency virus; HIV-LP; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-MAY-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9400562-A.
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ilarity 100.0%;
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Pred. No.
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                                                                                                                                              Query Match
Best Local S
Matches 28
                                                                                                                                                                                                               A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences or given in T19001-T25837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-oriented cDNA by using poly(T) as the sole primer. Since the 3'-outranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency off a given GS in a cDNA library can be determined (sep. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for sequence 51 BP; 14 A; 16 C; 12 G; 9 T;
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Best Local S
Matches 28
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                                                                                                                       16309 GCCCAGGCTGGAGTGCAGTGGCGTGATC 16336
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Human gene signature HUMGS07164.
Gene signature; messenger RNA; mRNA; relative abundance; frequency; human; cloning; mapping; non-biased library; diagnosis; detection; cell typing; abnormal cell function; ss.
HOMO Sapiens.
NO9514772-A1.
01-JUN-1993, JD-355504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reducing conditions, respectively) and an N-terminal sequence as R79913 is claimed. The polypeptide was isolated from human 198G cells and is useful for treating pancreatitis, shock, multiple organ failure and disseminated intravascular coagulation. The present sequence is that of an antisense primer used for cloning 198G cDNA coding for the full-length polypeptide. Sequence 48 BP; 2 A; 1 C; 1 G; 44 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Matsubara K, Okubo K; MPI; 95-206931/27. When; 95-206931/27. Identifying gene signatures in 3'-directed human cDNA library - Identifying gene signatures in 3'-directed human cDNA library - for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
Q95177 standard; DNA; 57 BP
Q95177;
08-FEB-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 1755; 2245pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25038 standard; cDNA to mRNA;
                                                                                            28 GCCCAGGCTGGAGTGCAGTGGCGTGATC 1
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28; Conser
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ilarity 100.0%;
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Pred. No.
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                                                                                                                                     Query Match
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Matches 28
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                 60 AAAAAAAAAAAAAAAAAAAAAAAAA 33
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Oy 16309 GCCCAGGCTGGAGTGCAGTGGCGTGATC 16336
24.APR.1997.

24.APR.1997.

18.CCT.1995; U16637.

PR 19.CCT.1995; U5-005598.

PR 19.CCT.1995; U5-005598.

AXEL R. DUIAC C;

DNIV COLUMBIA NEW YORK.

PA (VYCO) UNIV COLUMBIA NEW YORK.

PR NO. DUIAC C;

DNIV COLUMBIA NEW YORK.

PR NO. DUIAC C;

PR WPI; 97-245107/22.

PR WPI; 97-245107/22.

PA (VYCO) UNIV COLUMBIA NEW YORK.

PT useful to identify modulators for control of reproductive and social behaviour, fertility and hormone secretion

PT useful to identify modulators for control of reproductive and social behaviour, fertility and hormone secretion

PT useful to identify modulators secretion

PD 105closure; Page 50; 123pp; English.

PD 105closure; Page 50; 123pp; English.

PO 105closure; Page 50; 123pp; English.

PT useful to identify and hormone secretion rat

PT useful to identify modulators secretion

PT useful to identify modulators for control of sequences in the meurons.

PA (VIC) PA (VIC)

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PA (VIC) PA (VIC)

PT useful to identify modulators for control of actions of
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Best Local Similarity 100.0%;
Matches 28; Conservative (
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Q95177 is a simple tandem repeat (STR) corresponding to the 2nd part of wgla2. The STR can be used for treatment and diagnosis in human and veterinary medicine, partic. for genetic characterisation, mapping, linkage studies and analysis/diagnosis of acquired disease alleles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JUN-1995.
21-DEC-1994; G02789.
21-DEC-1993; GB-026052.
21-DEC-1993; GB-026052.
(UYLE-) UNIV LEICESTER.
Armout J. Jeffreys AJ;
WPI; 95-240682/31.
Identifying simple tandem repeat loci in DNA - by screening DNA ilbrary to enrich for fragments contg. the repeats before cloning and rescreening, also simple tandem repeats for treatment or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pheromone receptor; vomeronasal sensory neuron; social behaviour; maternal behaviour; reproductive behaviour; fertility; hormone secretion; polymerase chain reaction; PCR; primer; ss.
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Synthetic.
W09714790-A1.
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Synthetic.
WO9517522-A2.
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69401 standard; DNA; 60 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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Pred. No. 15
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Similarity

0.1%; ilarity 100.0%; Conservative

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Score 28; DB Pred. No. 15; 0; Mismatches

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RESULT
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 닭
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PT useful in medical diagnosis

PT claim 2; Page 11; 15pp; English.

CC The sequence is an example of a preferred T7 RNA polymerase of the sequence is an example of a preferred to the 3' end of the promoter for use in the invention. There can be from 2 to 50 T's in the loop region. A probe sequence is ligated to the 3' end of the promoter region. Upon hybridisation of the probe to a target sequence and ligation of the hybridisation of the probe to a target sequence and ligation of the hybridisad target sequence to the 5' end of the CC and ligation of the hybridisad target sequence to the 5' end of the CC hairpin-forming sequence, the target sequence to be amplified CC and detected) using a single oligonucleotide component (c.f. PCR).

See also Q11759 and Q11761-Q11764.

So Sequence 86 BP; 12 A; 6 C; 6 G; 62 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 28
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15-MAY-1991.
27-OCT-1990; 120650.
09-NOV-1989; US-434372.
23-AUG-1990; US-569991.
(MOLE-) MOLECULAR DIAGNOSTI.
                                                                                                                                                                                                                                                                                                                                                                                                                                  29692
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Self-complementary, T7 promoter hairpin-forming
T7 bacteriophage; DNA-dependent RNA polymerase;
                                                                                                                                              10-DEC-1998.
05-JUN-1998; U12141.
05-JUN-1997; US-048662.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dattagupta N;
WPI; 91-141638/20
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                                                       New recombinant porcine reproductive and respiratory syndrome virus - containing nucleic acid encoding a polymerase from an RNA virus and open reading frames 2-7 of the porcine virus, used particularly
                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                    Porcine reproductive and respiratory syndrome virus PCR primer PRRSV-2. Equine arteritis virus; EAV; vaccine; structural gene; PRRSV; porcine reproductive and respiratory syndrome virus; recombinant virus;
                                                                                                                                                                                                                                                                                                                               X00174 standard;
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The present inve
polymerase from
                                                                                                     Coussens PM, Reilly JD, WPI; 99-080829/07.
                                                                                                                                                                                           WO9855626-A2.
                                                                                                                                                                                                                                     PCR primer; ss.
                              Example 2; Page 21;
                                                                                                                                  (ORIG-) ORIGEN INC.
                                                                                                                                                                                                         Porcine reproductive
                                              in vaccines
                                                                                                                                                                                                                                                                                                23-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                      73
                                                                                                                                                                                                                                                                                                                                                                                                    sequence amplification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 100
28; Conservative
invention de from an RNA
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/note=
                                                                                                                                                                                                                                                                                                                               DNA;
                           55pp;
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describes a nucleic acid which encodes A virus, excluding porcine reproductive
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"number of T's
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                                                                                                                                                                                                          respiratory syndrome virus
                              English.
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Pred.
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T23178
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Best Local S
Matches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Preparation of yeast artificial chromosomes by in vivo recombination using vector comprising yeast centromere, marker, recombination using vector comprising yeast centromere, marker, yeast telomere and nucleic acid for recombination

Example 1; Page 45; 117pp; English.

This is the nucleotide sequence for the PCR primer used in the All repeat sequence, which is used to demonstrate the processes described in the invention. It involves the creation and use of circular yeast artificial chromosome (YAC) to selectively clone specific nucleic acids from a background of mixed nucleic acids by introducing the vector(s) into E. coli cells. They can be used to rapidly isolate human DNA where only a part of the sequence of DNA is known. Using the methods large fragments of DNA can be easily cloned and analysed.

Sequence 40 BP; 7 A; 12 C; 13 G; 8 T;
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Best Local S
Matches 28
                                                                                                                                                                                                                                                                                                15-JAN-1998.
09-JUL-1996; U11478.
09-JUL-1996; WO-U11478.
(USSH ) US DEPT HEALTH & HU
KOUPTINA NY, LATIONOV VL, P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29696 AAAAAAAAAAAAAAAAAAAAAAAAAAA 29723
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30-AUG-1996 (first entry)
Human gene signature HUMGS04920.
Gene signature; messenger RNA; mRNA;
human; cloning; mapping; non-biased
cell typing; abnormal cell function;
                                                                                                                                       T23178
T23178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              respiratory syndrome virus (PRRSV), and open reading frames (ORFs) 2-7 of PRRSV. The use of a polymerase gene from RNA viruses can provide for production of less mutagenic recombinant viruses. The recombinant viruses can be used in vaccines which have a reduced risk of loss or reduction of efficacy. The vaccines are used particularly for protecting swine against PRRSV. The high fidelity RNA polymerase gene can be used as a marker that allows organisms vaccinated with such a vaccine to be distinguished from organisms naturally infected with wild type strains of virus or other vaccines. The present sequence represents a PCR primer used in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces sp
WO9801573-A1.
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                                                                                                                                                                standard;
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                                                                                                                                                                                                                                                                                                                                                                                                            27;
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VL, Perkins EL, Resnick MA;
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Pred. No. 13;
0; Mismatches
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                   ВP
                           relative abundance; library; diagnosis;
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13;
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                                 detection;
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RESULT 10
V37197/c
TD V37197
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PT Virus containing nucleic acid and protein sections - for use in windification and creation of functional bio:polymers such as renzymes, antibodies and ribozyme(s)
PT enzymes, antibodies and ribozyme(s)
PS Example 1; Page 44; 68pp; Japanese.
CThe present sequence is used in the course of the invention. The specification describes a molecule for bringing together genotype with phenotype (in vitro virus). The molecule contains a nucleic acid phenotype (in vitro virus). The molecule contains a nucleic acid fragment having a base sequence corresponding to a genotype, covalently completed to a protein fragment containing a protein participating in phenotype expression, the 3'-end of the nucleic acid part being bonded to the C-terminus of the protein part via a puromycin molety. The nucleic acid fragment preferably consists of RNA corresponding to the gene (free adapter (such as a DNA-tRNA hybrid containing an anticodon corresponding to the terminator codon of the gene) and a puromycin-containing cap capable of binding to an amino acid residue. Translation of the virus is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences of in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences of as a means of diagnosing abnormal cell function or for sequences as a means of diagnosing abnormal cell function or for Sequence 61 BP; 23 A; 12 C; 14 G; 12 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18097 GATCACGCCACTGCATTCCAGCCTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
MATSUBARA K, Okubo K
MPI; 95-206931/27.
                                                                                                                                                                                                                                                                                                                                                         (MITU ) MITSUBISHI CHEM CORP. Fusimi Y, Miyamoto E, Nemoto N, Yanagawa H; WPI; 98-261039/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-SEP-1998 (first entry)
Oligonuclectide sequence of the specification.
Genotype; phenotype; molecular evolutionary engineering;
functional biopolymer; virus; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 1305; 2245pp; Japanese.
A single-stranded DNA (or its complem
                                                                                                                                                                                                                                                                                                                                                                                                                          23-APR-1998.
17-OCT-1997; J03766.
17-OCT-1996; JP-274855.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GATCACGCCACTGCATTCCAGCCTGGG 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; DNA;
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l Similarity 100.0%;
27; Conservative
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Pred. No.
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29;
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Query Match Best Local S Matches 27

. Similarity 27; Conserv

0.1%;

Score 27; DB; Pred. No. 26; 0; Mismatches

DB 1; 26;

Length 88;

0;

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RESULT
V39744
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PT Sequencing nucleic acid by mass spectrometric analysis - for Sequencing nucleic acids, telomerase activity, oncogene mutations, or PT cancer-specific sequences, for diagnosis of disease
PS Example 11; Page 318; 478pp; English.

CA process has been developed for determining the sequence of a target cucleic acid. The process comprises: (1) generating at least two fragments (F) from the target nucleic acid; and (ii) analysing F by CC mass spectrometry (MS). The sequences in V39483 to V39592 are specifically claimed primers for use in the mass spectrometric analysis CC of the above process. The process is used to detect genetic diseases (e.g. haemophilia, thalassemia, Duchenne muscular dystrophy, Alzheimer's CC (e.g. haemophilia, thalassemia, Duchenne muscular dystrophy, Alzheimer's CC (or predisposition); infections and cancers; also for establishing CC identity and heredity. Particular applications are diagnosis of neuroblastoma, detecting telomerase, determining family relationships CC and HLA compatibility, and in genetic fingerprinting. Compared with CC known methods using MS, this process requires fewer specific reagents CC and HLA compatibility and in genetic fingerprinting. Compared with CC known methods using MS, this process requires fewer specific reagents and is better suited to automation. Extended primers are shorter; and is better suited to automation and the process allows detection of CC many sequences simultaneously. The present sequence represent an CC oligonucleotide used in an example from the present invention.

Sequence 88 BP; 56 A; 5 C; 7 G; 20 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cancer specific sequence;

Synthetic.

WO9820166-A2.

14-MAY-1998.

06-NOV-1997; US-947801.

06-NOV-1996; US-74448.

06-NOV-1996; US-744636.

06-NOV-1996; US-746036.

06-NOV-1996; US-746036.

06-NOV-1996; US-746036.

05-NOV-1996; US-746036.

23-JAN-1997; US-786988.

23-JAN-1997; US-78638.

23-JAN-1997; US-787639.

19-SEP-1997; US-93393.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      performed in a non-cellular (preferably ribosomal) system (e.g. E. coli ribosome), the protein synthesised by the translation attaching to the puromycin cap, resulting in the complete in vitro virus structure. The method is used in molecular evolutionary engineering to optimise function of a functional biopolymer such as an enzyme, antibody or ribozyme, or to generate new functionality. The virus can be used for the functional optimisation of nucleic acid or protein sequences.

Sequence 80 Bp; 7 A; 10 C; 1 G; 62 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-SEP-1998 (first entry)
MicrosateLilite analysis antisense strand SEQ ID NO:262.
MicrosateLilite analysis antisense strand SEQ ID NO:262.
Mass spectrometry; diagnosis; detection; biological sample; genetic disease; chromosomal abnormality; identification; he pathogenic organism; telomerase activity; oncogene mutation; cancer-specific sequence; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SEQU-) SEQUENOM INC.

Braun A, Damhoffer Denar B, Fu D, Higgins GS, Jurinke
Braun A, Little DP, Lough DM, Siegert CW, Tang K,
Van Den Boom D, Xiang G;
WPI; 98-286975/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66
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nes 27; Conserv
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pred. No. 27;
s; Pred. No. 27;
smatches
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27;
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S

23274 AAAAATAAATAAATAAATAAATAAATA 23300

AAAAATAAATAAATAAATAAATA 41

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RESULT
Q75099,
ID Q7
AC Q7
DT 11
DE P7
KW P8
                                                                                                                                                                                                                                                                                                                                                                                                             CC The present invention describes a method for detecting a target nucleic cc acid sequence (I) in a sample. The method comprises: (a) hybridising (I) CC to the probe ends of a probe having 2 free nucleic acid end parts, which cc are at least partially complementary to and capable of hybridising to CC at least 2 neighbouring regions of (I); (b) covalently connecting the cends of the hybridised probe with each other to form a circularised CC structure; (c) washing under denaturing conditions, characterised in that the probe is provided with a cleavable or dissociable detectable function; (d) cleaving or dissociating the detectable function; (e) CC separating probes with connected ends from probes with non-connected ends by washing under denaturing conditions; and (f) detecting the presence and, if desired, location of the remaining probe as indicative of the presence of (I). The present sequence represents a padlock probe, can be used to detect, quantify and distinguish between sequence variants with regard to 1 or several (I) in a sample. It can be used to disease, for genetic linkage analysis of biallelic markers and to consect that it reports the presence of (I) by allowing a detectable consisting to remain bound only if the probe has been cyclised in a target dependent linking reaction. It also provides for high specificity and consecuence of the presenticity and capable to be a consecuence of the presence of (I) by allowing a detectable consisting the probe has been cyclised in a target dependent linking reaction. It also provides for high specificity and consecuence of the presenticity and capable to be a consecuence of the presenticity and capable to be a consecuence of the presenticity and capable to be a consecuence of the presenticity and capable to be a consecuence of the presenticity and capable to be a consecuence of the presenticity and capable to be a consecuence of the presenticity and capable to be a consecuence of the presenticity and capable to be a consecuence of the presenticity and capable 
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                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 27
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12-MAY-1998 (first entry)
12-MAY-1998 (first entry)
                                                                               075099 standard; cDNA;
075099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Padlock probe alphaFV from WO9741254.
Cleavable padlock probe; target nucleic acid;
circularised structure; hybridisation; Factor
Plasmid pOKSC18a contg. portion of psychosis protecting protein; PCR; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Fig 7; 20pp; English.
The present invention describes a method for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detecting target nucleic acid sequence - using probe forming circularised structure, which can be cleaved detectable function
                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                           background
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9741254-A1.
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                                                                11-AUG-1995
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30-APR-1996;
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                                                              (first entry)
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/note= "attached to an amino group'
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                                       protecting protein
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V; ss.
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Query Match Best Local S Matches 27

on 0.1%; S l Similarity 100.0%; 27; Conservative 0;

Score 27; DB Pred. No. 25; 0; Mismatches

25

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Box MPI: 98-557473/47.

Box MPI: 98-557473/47.

Box DNA sequences isolated from endogenous human retroviral element related vectors, transformed cells, proteins and antibodies, proteins and related vectors, transformed cells, proteins and antibodies, proteins and related vectors, treatment and prevention of breast cancer useful for diagnosis, treatment and prevention of breast cancer.

Claim 1; Page 47; 173pp; English.

Colaim 1; Page 47; Page 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acids encoding psychosis protecting peptide and antibodies - for the treatment, diagnosis and research of psychotic disorders, such as schizophrenia Claim 1; Page 52; 87 pp; English.

A subtracted cDNA library was generated from the RNA of lymphocytes obtd. from monozygotic twins discordant for schizophrenia. The two oligos used in library construction were T7 promoter and SP6 promoter (see Q75091, Q75092). A cDNA library was made for each twin and subtractive hybridisation was achieved. Both libraries were used as driver and substrate in two separate subtraction assays. Clone pOKS18a was isolated and sequenced. Sequence 95 BP; 12 A; 14 C; 30 G; 39 T;
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24-NOV-1994.
13-MAY-1994;
13-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA molecule encoding a breast tumour specific polypeptide #19. Human; breast cancer; breast tumour tissue; diagnosis; treatmen vaccine; epitope; endogenous; retroviral element; ss. Homo sapiens.

MO9845328-A2.
                                                                                                                                                                                                                                                                                                                                                                                             09-APR-1998; U06939.
11-DEC-1997; US-991789.
09-APR-1997; US-838762.
(CORI-) CORIXA CORP.
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misc_difference
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Pred. No. 26;
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V71935/c
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AC V719
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DI 18-F
DI 19-N
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Search completed: March 31, 2000, 00:01:30 Job time: 159088 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC V71935 standard, DNA; 27 BP.

AC V71936; DNA; 115ra primer.

AND V71936; DNA; 115ra primer.

AND V71936; Screening, Mybridisation; nucleic acid amplification; with immobilise; screening, Mybridisation; nucleic acid amplification; Synthetic.

AND V71938; DNC186.

BY Synthetic.

BY Synthetic.

BY NOV-1998; DNC-00643.

BY NOV-1998; DNC-00643.

BY NOV-1998; DNC-00643.

BY PR 13-NAY-1999; DNC-006447.

BY PR 1
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Best Local Similarity 100.0%; Pred. No. 67;
Matches 26; Conservative 0; Mismatches 0; Indels
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20, Appl
20, Appl
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21, Appl
22, Appl
37, Appl
37, Appl
38, Appl

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Post-processing: Listing first 45 summaries
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length: 105
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Match
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                                                 GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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/cgn_2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn_2_6/ptodata/1/ina/5D_COMB.seq:*
/cgn_2_6/ptodata/1/ina/5D_COMB.seq:*
/cgn_2_6/ptodata/1/ina/5D_COMB.seq:*
/cgn_2_6/ptodata/1/ina/peruy9_ComB.seq:*
/cgn_2_6/ptodata/1/ina/backfiles1.seq:*
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US-08-454-557C-57

US-08-450-673C-57

US-08-450-673C-57

US-08-454-557C-69

US-08-450-673C-69

US-08-450-673C-69

PCT-US95-17111A-69

US-08-233-609-5

US-08-233-609-5

US-08-233-609-5

US-08-242-745-5

US-08-443-129-5

US-08-443-129-5

US-08-443-130-5

PCT-US95-04467-5

US-08-332-766A-3

US-08-325-886-10

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                 sequence
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69, Appl
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US-08-454-557C-57
. Sequence 57, App
                                δÃ
                                                                                                                                                 US-08-454-557C-57
                                                                                                                                                                                             APPLICATION NUMBER: US/08/454,557C
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: LUGW19, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840003
REFERENCE/DOCKET NUMBER: 0609.3840003
TELEPHONE: (202) 371-2560
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 base pairs
TYDE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 57 Patent No.
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Matches 38
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CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIT: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
TENDET APPLICATION DATA:
TOTAL TOTAL STATE OF THE AMERICAN STATE
CURRENT APPLICATION DATA:
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   APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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US-08-113-646A-40
US-08-222-177A-349
US-08-378-494B-114
US-08-381-572-20
US-08-381-572-20
US-08-653-823B-72
US-08-653-823B-72
US-08-653-823B-72
US-08-778-494B-111
US-08-778-494B-111
US-08-522-269B-18
US-08-522-269B-18
US-08-522-269B-18
US-08-778-494B-16
US-08-778-494B-16
                                                                                Score 38; Pred. No.
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Detection

Result No.

Score

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Gaps

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Minimum DB Maximum DB

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Word size Searched:

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Perfect score: Sequence:

Title:

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Scoring table:

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US-08-340-426D-57; Sequence 57, Application US/08340426D; Patent No. 5948634
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US-08-450-673C-57
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Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                         Sequence 57, Application US/08450673C Patent No. 5948888 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEPAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 57:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340
FILING DATE: 14 NOV-1994
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: LUdwig, Steven R. 0.3
REGISTRATION NUMBER: 36.03
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LENGTH: 60 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                           APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
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                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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ZIP: 200
                                                                                                                         STREET: 1100 New CITY: Washington
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                                                                      ZIP: 20005-3934
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                                                                                                                                                                        ADDRESSEE:
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                                                                                                             D.C.
                                                                                                                                                   E: Sterne, Kessler, Goldstein & Fox P.L.L.C. 1100 New York Avenue, Suite 600
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100.0%; Pred. No. 0.00064;
ative 0; Mismatches 0;
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         PCT-US95-17111A-57
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                                                                                                                                TELEFAX: (202) 371-25
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340,425
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                        NAME: Ludwig, Steven R.
REGISTATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                           SEQUENCE CHARACTERISTICS:
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                                            STRANDEDNESS:
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Qy 17232 TTTTTGTATTTTTAGTAGAGACAGGGTTTCACCGTGTT 17269
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; Sequence 57, Application PC/TUS9517111A
; GENERAL INFORMATION:
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Best Local Similarity
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NFORMATION FOR SEQ ID NO:
                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
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LENGTH: 60 base pairs
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REGISTEATION NUMBER: 36,203
REGISTEATION NUMBER: 06/
REFERENCE/DOCKET NUMBER: 06/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 30-MAY-19
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                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Neural Thread Protein Gene Expression TITLE OF INVENTION: Detection of Alzheimer's Disease NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                          NPPLICANT: de la Monte,
NPPLICANT: Wands, Jack R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 TTTTTGTATTTTAGTAGAGACAGGGTTTCACCGTGTT 53
                                                                                                                                                      COUNTRY: U.S.A.
ZIP: 20005-3934
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SOFTWARE: PatentIn Release #1.0, Version #1.25
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APPLICATION NUMBER:
                                                                                                                                                                                                                    ITY: Washington
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; Pred. No. 0.00064;
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RESULT 6
US-08-340-426D-69
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                                                                           Sequence 69, Application US/08340426D Patent No. 5948634
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Best Local
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GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (202) 371-254
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/01
FILING DATE: 30-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: NEITITLE OF INVENTION: OF NUMBER OF SEQUENCES: 1: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: de la Monte, S
APPLICANT: Wands, Jack R.
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                     TTTTTGTATTTTAGTAGAGACAGGGTTTCACCGTGTT 53
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100.0%; Pr
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0; Mismatches
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Pred. No.
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hes 0;
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US-08-450-673C-69
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                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Ver:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,673C
FILING DATE: 30-MAY-1995
RAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0605
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
TELEFAX: (202) 371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17232 TTTTTGTATTTTTAGTAGAGACAGGGTTTCACCGTGTT 17269
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INFORMATION FOR SEQ ID NO:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,426D
FILING DATE: 14-NOY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression
TITLE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                 CLASSIFICATION: 530 ATTORNEY/AGENT INFORMATION:
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ZIP: 200
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STREET: 11
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ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                             CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Ludwig, Steven R. REGISTRATION NUMBER: 36,203
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100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69:
                                                               0609.3840004
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                                                                                                                                                                                                                Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.00061;
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69:

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RESULT 9
US-08-233-609-5/c
                                                                                                                         OY 17232 TTTTTGTATTTTTAGTAGAGACAGGGTTTCACCCGTGTT 17269
                                                                                                                                                                                                                                                                                                           PCT-US95-17111A-69
                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/340,426
APPLICATION UNMBER: 08/340,426
APTORNEY/ACENT INFORMATION:
NAME: Lidwig Steven R.
REGISTRATION UNMBER: 36,203
REFERENCE/DOCKET UNMBER: 0609.3840002
TELECOMMUNICATION INFORMATION:
TELEPAX: (202) 371-2600
TELEPAX: (202) 371-2600
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARGIERISTICS:
LENGTH: 76 base pairs
TYPE: nor-laif acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QY 17232 TTTTTGTATTTTTAGTAGAGAGAGGGTTTCACCGTGTT 17269
                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                              Query Match
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ECT-US95-17111A-69

Sequence 69, Application PC/TUS9517111A

GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 76 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and
TITLE OF INVENTION: Detection of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                       16 TITTIGTATITTTAGTAGAGACAGGGTTTCACCGTGTT 53
                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1100 New CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 TTTTTGTATTTTTAGTAGAGACAGGGTTTCACCGTGTT 53
                                                                                                                                                                                    .ch 0.1%; Score 38; DB 6; I
Il Similarity 100.0%; Pred. No. 0.00061;
38; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D.C
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                                                                                                                                                                                                                            Length 76;
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                                                                                                     RESULT 10
US-08-44-083-5/c
; Sequence 5, Application US/08444083
Patent NO. 5571675
; GENERAL INFORMATION:
APPLICANT: Baker, Joffre
APPLICANT: Chien, Kenneth
APPLICANT: Fing, Kathleen
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Wood, William
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOSTWARE: Patth (Genentech)

SOSTWARE: Patth (Genentech)

APPLICATION NUMBER: US/08/233,609

FILING DATE: 25-APR-1994

CLASSIFICATION: 435

PRIOR APPLICATION NUMBER:

FILING DATE: 15-APR-1994

CLASSIFICATION NUMBER: 28,616

PRIOR APPLICATION UMBER: 28,616

REFIERENCE/AGENT NUMBER: 28,616

REFIGERATION NUMBER: 894

TELEPAN: 415/925-1896

TELEPAN: 415/925-1896

TELEPAN: 415/925-1896

TELEPAN: 910/371-7168

INFORMATION FOR SEO ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 50 bases

TYPE: nucleic acid

STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
US-08-233-609-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 0.1
Best Local Similarity 100.
Matches 28; Conservative
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/08233609 Patent No. 5534615 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Baker, Joffre
APPLICANT: Chien, Kenneth
APPLICANT: King, Kathleen
APPLICANT: Pennica, Diane
APPLICANT: Pennica, Diane
APPLICANT: Wood, William
ITILE OF INVENTION: Cardiac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS: ADDRESSE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.1%; Score 28; DB 1; Length 50;
100.0%; Pred. No. 1.3;
tive 0; Mismatches 0; Indels
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COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 in

PC-DOS/MS-DOS

360 Kb floppy disk

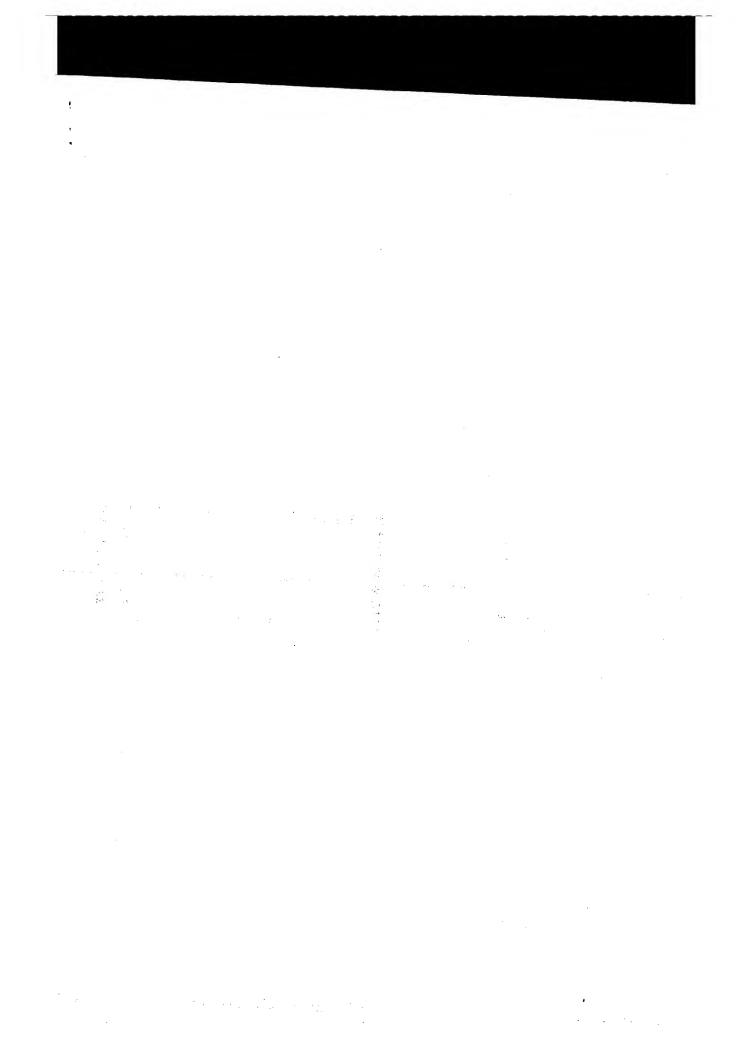
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/08286304 Patent No. 5571893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/233609
FILING DATE: 25-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/286304
FILING DATE: 05-AUG-1994
FILING DATE: 05-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: TORCH1A, Timothy E:
REGISTRATION NUMBER: 36,700
REGISTRATION NUMBER: 894P1D5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEPHONE: 415/225-8674
PRING DATE: 455
CLASSIFICATION: 455
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/233609
APPLICATION NUMBER: 25-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29696 AAAAAAAAAAAAAAAAAAAAAAAGAAT 29723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA: US/08/286,304
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wood, William
TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
TUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS ""
SOFTWARE: pa+1-
TRRPP"
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                                                                                                            APPLICATION NUMBER: US/O
FILING DATE: 05-AUG-1994
                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 50 bases
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08 FILING DATE: 17-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                             SSEE: Genentech, Inc.
T: 460 Point San Bruno Blvd
South San Francisco
California
                                                                                                                                                                                                                                                                            94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baker, Joffre
Chien, Kenneth
King, Kathleen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pennica, Diane
                                                                                                                                                                                                                                                                                            USA
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US-08-442-745-5/c
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Best Local S
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                                                                                                                                                                                                APPLICATION NUMBER: US/08/442,745
FILING DATE: 17-may-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/233609
FILING DATE: 25-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/286304
FILING DATE: 05-AUG-1994
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 50 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Baker, Joffre
APPLICANT: Chien, Kennet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      equence 5, Application US/08442745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wood, William
TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor NUMBER OF SEQUENCE: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                        REFERENCE/DOCKET NUMBER: 89
TELECOMMUNICATION INFORMATION:
                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,7
                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 AAAAAAAAAAAAAAAAAAAAAAAA 17
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech)
                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX:
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REFERENCE/DOCKET NUMBER:
                                                     ELEFAX: 415/952-9881
ELEX: 910/371-7168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94080
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Similarity 100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 King, Kathleen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pennica, Diane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kenneth
                                                                                                                             36,700
R: 894P1D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 50;
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OY 29696 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 29723
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MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER STEEM: PC.DOS/MS-DOS
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/443,129
ETLING DATE: 17-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/233609
PRIOR APPLICATION UNMBER: 08/233609
PRIOR APPLICATION UNMBER: 08/23609
PRIOR APPLICATION UNMBER: 08/286
FILING DATE: 25-APR-1994
APPLICATION NUMBER: 304
FILING DATE: (0-8)
APPLICATION NUMBER: 304
FILING DATE: (0-11)
ATTORNEY_AGENT INFORMATION:
NAME: TOTCHA: 71mcthy E.
REGISTRATION NUMBER: 36,700
REFERENCE_POCKET NUMBER: 36,700
REFERENCE_POCKET NUMBER: 36,700
REFERENCE_TOCKET NUMBER: 
                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
US-08-443-129-5
                                                                                                                                                                                                                          Query Match
Best Local (
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US-08-443-129-5/c
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US-08-442-745-5
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GENERAL INFORMATION:
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ADDRESSEE: Geneatech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
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APPLICANT: Chien, Kenneth
APPLICANT: King, Kathleen
APPLICANT: Pennica, Diane
APPLICANT: Wood, William
TITLE OF INVENTION: Cardiac Hypertrophy Factor and Uses Therefor
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U
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                                                                                                                                            ch 0.1%; Score 28; DB 1; Length 50; l Similarity 100.0%; Pred. No. 1.3; 28; Conservative 0; Mismatches 0; Indels
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5, 5627073
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MEDIUM TYPE: 5.25 Inch, 360 Kb floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/08/443,952
FILING DATE: 17-MAY-1995
CLASSIFICATION NUMBER: 08/233609
FILING DATE: 17-MAY-1994
APPLICATION NUMBER: 08/233609
FILING DATE: 25-ARR-1994
APPLICATION NUMBER: 08/26304
APPLICATI
                                                                                                                                                                                                                                                                                                                                                                                                         US-08-443-130-5/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
US-08-443-952-5
                                                                                                                                                                                                                  Sequence 5, Application US/08443130 Patent No. 5723585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 0.1%; Score 28; DB 1; Length 50; Best Local Similarity 100.0%; Pred. No. 1.3; Matches 28; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                      Patent No. 5723585
GENERAL INFORMATION:
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TITLE OF INVENTION: CE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Baker, Joffre APPLICANT: Chien, Kenneth APPLICANT: King, Kathleen APPLICANT: Pennica, Diane APPLICANT: Wood, William
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STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
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Baker, Joffre
Chien, Kenneth
King, Kathleen
Pennica, Diane
Wood, William
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Matches ;



Title:
Perfect score:
Sequence:

Run on:

Scoring table:

Minimum DB Maximum DB

Word size : Searched:

Database

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Post-processing: Listing first 45
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13816.022 Million cell updates/sec
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gb_est1: *

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AQ280224 CITBI-E1-
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Use of a random human BAC End Sequence Databas Map Building
Unpublished (1998)
Other_GSSs: CITBI-E1-2522N7.TR
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850,
                                                                                                                                                                                                                              human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;

Eukherja; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 101)

Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,

Yenter,J.C.

Yenter,J.C.
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AA63125 zs94e0.s

AA65098 unv6d11.s

B63983 unv6d11.s

B63983 unv6d1.s

B63983 unv6d0.s

AA807640 nx08b05.s

AA807640 nx08b05.s

AA807640 nx08b05.s

AA807640 nx08b01.s

A1206968 qr30g11.x

AA501753 ng05a01.s

A2291270 zs18d04.s

T52775 yn79d08.r1

AA53875 nh32a06.s

AA835205 ak64h01.s

AA835205 ak64h01.s

AA835205 ak64h01.s
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H92864 yt91c11.s1
AA281256 zs94e09
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AQ319270 RPCII1-98
AA654562 nt75f10,8
AQ584425 RPCI-11-4
AA458985 ZX88h08.s
F26823 HSPD14446 H
AA570476 nk63h12.s
B90619 CITHSP-216
AQ535244 RPCI-11-3
D20989 HMMGS01071-3
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T52775 ya79d08.r1
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COMMENT
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AUTHORS
TITLE
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AI168167/c
LOCUS
DEFINITION
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Db 70 CAGTGGCTCACACCTGTAATCCCAGCACTTTGGGAGGCCAAGGT 27
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RS NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), National Cancer Institute, Cancer Genome Anatomy Project (CGAP), On Jan 19, 1998 this sequence version replaced gi:2282306.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov

This clone is available royalty-free through LLNL; contact the Insert Length: 1481 Std Error 10.00

Insert Length: 1481 Std Error 0.00

Seq primer: -40ml3 fwd. Er from Amersham

Location/Qualifiers

urce
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93 bp mRNA

0009e10.x1 Soares_NSF_F8_9W_OT_PA_P_S1 Homo sapiens CDNA Clone
IMAGE:1565706 3' similar to contains Alu repetitive
element; contains TAR1 repetitive element ;/ mRNA sequence.
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Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Class: BAC ends.
/note="Top and pooled; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Ecc RI; Equal amounts of plasmid DNA from five normalized 11braries were mixed, and ss circles were made in vitro. A subtractive hybridization, this DNA was used as tracer in PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries The pools consisted of the following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                    /Organism-"Homo Sapiens"
/db_Xref-"taxon:9606"
/clone="IMAGB:1565706"
/clone=11b-"Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host-"DBH10B"
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1. 101
/organisme Homo sapiens // db_xref="taxon:9606" // Clone="3522N7"
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/Gell_type="sperm"
/note="Vector: pBeloBaCll; Site_1: EcoRI; Site_2: EcoRI;
CalTech Human BAC Library D"
28 c 24 g 25 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="CITBI-E1"
/sex="male"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ); Score 44; DB 100; L
)%; Pred. No. 0.00059;
Mismatches 0;
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JOURNAL COMMENT

TITLE

REFERENCE AUTHORS

ACCESSION VERSION SOURCE ORGANISM

KEYWORDS

DEFINITION RESULT 1 AQ280224/c LOCUS

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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTGCAGTGAGCCGAAATCGCGCCACTGCACTCCAGCCTGGGT 22481
                                                                                                                                                                                                                                                                                                                                                                       Insert Size: 1013
High qality sequence stops: 82 Source: IMAGE Consortium, clone is available royalty-free through LLNL; contact the Consortium (info@image.llnl.gov) for further information insert Length: 1013
Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chiasoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T52775 95 bp mRNA EST 06-FEB-1995 ya79d08.rl Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:67887 5' similar to contains Alu repetitive element, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Other_ESTs: ya79d08.s1
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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T52775
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/lab_host="SOLR cells (kanamycin resistant)"
//note="Organ: ovary; Vector: Bluescript SK; Site_1: EcoRI;
Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT.
Total ovary tissue, normal, caucasian. Average insert
size: 0.8 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5'
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                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="GDB:504144"
/db_xref="taxon:9606"
/clone="IMAGE:67887"
                                                                                              /dev_stage="49 year old"
/lab_host="SOLR cells (k
                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                    /clone_lib="Stratagene ovary (#937217)"
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Pred. No.
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0.0027;
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AA837701/c
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                                                         Matches
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25734 GAGAATCACTTGAACCTGGGAGGCAGAGGTTGCAGTGAG 25772
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                                                                         Local
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AA837701
AA837701.1
                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
On Jan 17, 1998 this sequence version replaced Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 97)
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oe06c02.s1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tissue Procurement: Chri
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insert Length: 451
                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                        ert Length: 451 Std Error: 0.00 primer: -40ml3 fwd. ET from Amers h quality sequence stop: 50.
                                                     0.1%;
llarity 100.0%;
Conservative
                                                                                                                                                                   13
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                                                                                                                                                                                 /note="Vector: pamp10; mRNA made from invasive ovarian tumor, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAATTCGGCACGAG 3′ ~3′ adaptor sequence:
CTCGAGTTTTTTTTTTTTTT 3′"
a 32 c 20 g 24 t
                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1385090"
/clone_11b="NCI_CGAP_Ov2"
                                                                                                                                                                                                                                                                          /lab_host-"DH10B"
                                                                                                                                                                                                                                                                                               /tissue_type="ovary"
                                                                                                                                                                                                                                                                                                                  /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97 bp mRNA EST 07-APR-1998 NCI_CGAP_Ov2 Homo sapiens cDNA clone IMAGE:1385090 contains element PTR5 repetitive element; mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GI:2912900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Christopher A. Moskaluk,
                                                     Score 39; DB 39; Pred. No. 0.024; 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>,,</u>
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; Pred. No.
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                                                                                                                                                                                                                                                         AA654562 102 bp mRNA EST 04-NOV-1997 nt75f10.sl NCI_CGAP_Pr3 Homo sapiens cDNA clone IMAGE:1204563 similar to contains Alu repetitive element;contains element MER22 repetitive element; mRNA sequence.

AA654562 TELEFORM TO THE TRANSPORT OF THE T
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Class: BAC ends
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Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Pieter de Jong
(pleter@dejong.med.buffalo.edu). Clones may be purchased from
(pleter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderlig) or from
Research Genetics (info@tresgen.com). BAC end search page:
Research Genetics (info@tresgen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Other_GSSs: RPCIII-98B22.TV
Contact: Shaying Zhao, William Nierman, Mark
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C. Use of human BAC End Sequences for Sequence-Ready Map Building
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Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 102)
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              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                               Homo sapiens
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/db_xref="GDB:7537293"
/db_xref="taxon:9606"
/clone="repoi-11-98822"
/clone=lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cell_type="Lymphocytes"
/note="Vector: pBACe3.5; Site_1: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
28 c 31 g 17 t
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Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,
M.D., Michael Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
CDNA Library Arrayed by: Genome Systems Genome Sequencing Center
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 102)
NCI-GAP http://www.ncbi.nlm.nih.gov/nciogap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Map Building
Unpublished (1997)
Other_GSSs: RPCI-11-458L2.TV
Contact: Shaying Zhao, William Nierman, Mark Adams
                                                                                                                                                                                                                                                                                                    Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                            Venter, J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
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/db_xref="taxon:9606"
/clone="IMAGE:1204363"
/clone_lib="NCI_CGAP_Pr3"
/sex="Male"
                                                                                                                                                                                                                                                                  Adams, M.D., Nierman, W., Malek, J., de Jong, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  histologically-determined to be fully malignant prostate cancer cells. Double-stranded cDNA was ligated to Ecorl adaptors, 5 cycles of PCR applied to the CDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally cloned. This library was constructed by David Krizman."

27 g 21 t
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/lab_host="DH10B"
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Pred. No.
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0.05;
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Best Local :
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                                            source
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                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 82)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylle,T., Waterston,R. and Wilson,R. Washu-Marck EST Project 1997

Unpublished (1997)

On Sep 12, 1996 this sequence version replaced gi:1395423.

Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA458985 82 bp mRNA EST 09-JUN-1997 zx88h08.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE.810879 3' similar to contains LTR5.t2 LTR5 repetitive element
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
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Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or f:
Research Genet cs (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                     Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                        IMAGE Consortium (info@image.llnl.gov) for Seq primer: -41ml3 fwd. ET from Amersham High quality sequence stop: 70.
                                                                                                                                                        Email: est@watson.wustl.edu
This clone is available royalty free through LLNL ; contact the
                                                                                                                                                                                                            Tel: 314 286 1800 Fax: 314 286 1810
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                                                               quality sequence stop:
Location/Qualifiers
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/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
27 c 31 g 22 t
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/clone="RPCI-11-458L2"
/clone_lib="RPCI-11"
/organism="Homo sapiens"
/db_xref="GDB:6041714"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="Male"
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0.05;
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MEDLINE
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                                                                                                                                                                                                                                                                                           source
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                                                                                                                                                                                                                                                                                                                 ABI Chromatograms and other information are http://grup.bio.unipd.it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              l (bases 1 to 85)
Lanfranchi,G., Muraro,T., Caldara,F., Pacchioni,B., Pallavicini,A.,
Pandolfo,D., Toppo,S., Trevisan,S., Scarso,S. and Valle,G.
Identification of 4370 expressed sequence tags from a
3'-end-specific cDNA library of human skeletal muscle by DNA
sequencing and filter hybridization
sequencing and filter hybridization
Genome Res. 6 (1), 35-42 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F26823 85 k
HSPD14446 HM3 Homo
                                                                                                                                                                                                                                                                                                                                                                             CRIBI Biotechnology Centre University of Padua
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On Mar 16, 1998 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F26823
                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Valle G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Ve
Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="pectoral muscle (after mastectomy)", /note="Vector: pcDNAII (Invitrogen); Site_1: BstXI; Site_2: NotI; The library was constructed by G. Lanfranchi. This library is not subtracted nor normalized. The first strand cDNA was primed with a biotinylated
                                ds cDNA was sonicated and size-selected in the range 350-550 bp. The 3' specific fragments were selected streptavidin coated magnetic beads, ligated to
                                                                                non-palindromic BstXI adapters, NotI digested and directionally cloned into BstXI-NotI cut pcDNAII
                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="s400060G10"
/clone_lib="HM3"
                                                                                                                                                                                                       /sex="female
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GI:4812449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="Female"
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/clone="IMAGE:810879"
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0.12;
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AA570476
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                                           50 TTGGCTCATGCCTGTAATCCCAGTACTTTGGGAGGCC 86
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37; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Insert Length: 2104 Std Error: 0.00 Seq primer: -40m13 fwd. ET from Amersham High quality sequence stop: 76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1997)
On May 8, 1995 this sequence version replaced gi:801194.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 103)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Arraying: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: WCI-GAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tissue Procurement: L. J
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /ww-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA Library Preparation: Stratagene, Inc., David B. Krizman,
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//db_xref="taxon.9606"
//db_xref="taxon.9606"
//clone=_lib="NACE_IOR827"
//clone=_lib="NCI_CGAP_Schl"
//tlssue_type="Schwannoma tumor"
//lab_host="Solx (kanamycin resistant)"
//note="Vector: Bluescript SR-; Site_1: EcoRI; Site_2: /note="Vector: Bluescript SR-; Frimer: Oligo dT-Two yooled bulk Schwannoma tumors. 5' adaptor sequence: 5'
GANTTCGGCACGAG 3' 3' adaptor sequence: 5'
GCCAGGTTTTTTTTTTTTTTTTTTTTT 3' Average insert size: 1.2 kb."
27 a 19 c 31 g 26 t
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100.0%; Pr
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Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Mammalia; Eutheria: Primates: Catarrhini; Hominidae: Homo.

1 (bases 1 to 103)
2hao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter,J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                             B90619 103 bp DNA GSS 25-JUN-199 CIT-HSP-2163G1.TR CIT-HSP Homo sapiens genomic clone 2163G1. genomic survey sequence.
                                                                                                                                                                                                                                      AQ535244 103 bp DNA GSS 18 RPCI-11-317H22.TV RPCI-11 Homo sapiens genomic clone RPCI-11-317H22, genomic survey sequence.
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Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Researc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1998)
Other_GSSs: CIT-HSP-2163G1.TF
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Use of a random BAC End Sequence Database for Sequence-Ready Map
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 103)
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Seq primer: M13 Reverse
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/sex="Male"
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/clone="2163G1"
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/note="Vector: pBeloBAC11; S1te_1: HindIII; S1te_2:
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Okubo, K., Fukushima, A., Yoshii, J., Niiyama, T., Kojima, Y.,
Yoshinari, H., Arimoto, J. and Matsubara, K.
Gene expression of human promyelocytic cell line HL60 before and after induction of differentiation. A new application of 3'directed
                                                                                                                                                                                                                                                                                                                                                                       cDNA sequencing Unpublished (1993) Contact: Okubo.K., Fukushima.A., Yoshii.J., Nilyama.T., Yoshinari.H., Arimoto.J. and Matsubara.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D20989.1 GI:504809
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HUMGS01971 Human promyelocyte
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Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                             Osaka University
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                          Institute for Molecular and Cellular Biology
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Location/Qualifiers
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Medical Center Dr., Rockville,
301 838 0200
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/cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
27 c 27 g 18 t
                                      /clone="mp0383"
/clone=lib="Human promyelocyte"
/note="Female, adult, cell_line =
promyelocyte."
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/db_xref="taxon:9606"
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/db_xref="GDB:7621533"
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Unpublished (1997)
On May 5, 1995 this sequence version replaced
Contact: Wilson RK
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High quality sequence stop: 97.
    Location/Qualifiers
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Insert Length: 758 Std Error: 0.00
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Fax: 314 286 1810
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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36; Conservative
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//note="Vector: pBluescript Sr.; Site_1: EcoRI; Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dT. Pooled
retinal tissue. Average insert size: 1.0 kb; Uni-ZAP XR
Vector; -5 adaptor sequence: 5 GAATTCGGCACGAG 3 ~3'
adaptor sequence: 5 CCCAACTTTTTTTTTTTTTTTTT 3'"
a 25 c 26 g 29 t
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/db_xref="taxon:9606"
/clone="IMAGE:838880"
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KEYWORDS
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VERSION
Search completed: March 30, 2000, 19:57:22 Job time: 146496 sec
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Local Similarity 100.0%; Pred. No. 0.59; Length 65;
Local Similarity 100.0%; Pred. No. 0.59;
hes 35; Conservative 0; Mismatches 0; Indels
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 65)

RS Mahairas,G.G., Zackrone,K.D., Smith,T., Tipton,S., Schmidt,S.,
Traicoff,R., Abajian,C., Blanchard,A., West,A. and Hood,L.E.
Construction of a Characterized Clone Resource for Genomic
Sequencing: Generation and Preliminary Analysis of 20,000 Sequence
Tagged Connectors
Inpublished (1997)
Contact: Mahairas GG, Zackrone KD, Hood L
University of Washington
Seattle, WA 98195, USA
Tel: (206) 816-8744
Fax: (206)
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B36140
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/db_xref-"taxon:9606"
/clone="plate=CT 820 Col=11 Row=G"
/clone_1ib-"CIT Human Genomic Sperm Library C"
/sex-"M"
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-6791.518 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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INITION	Human alpha-galactosidase breakpoint region.	region.	
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SION	M36131.1 GI:179541		

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  unidentified
                                                                     Sequence 2 from Patent WO9801573.
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Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 80)
Kornreich,R., Bishop,D.F. and Desnick,R.J.
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Kornreich, R., Bishop, D.F. and Desnick, R.J.

Alpha-galactosidase A gene rearrangements causing Fabry disease:
Identification of short direct repeats at breakpoints in an
                                                    A68622.1 GI:4759649
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Biol. Chem. 265, 9319-9326 (1990)
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HUMLDLRFL/c
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                                                                       Sequence 57 from patent US 5830670.
AR051487
AR051487.1 GI:5974851
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Chromosome 19p13.2-p13.1.
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1 (bases I to 40)
1 (bases I to 40)
Resnick, M.A., Larionov, V.L., Kouprina, N.Y. and Perkins, E.L.
TRANSPORMATION ASSOCIATED RECOMBINATION CLONING
PATENT: WO 9801573-A 15-JAN-1998;
US HEALTH (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clean copy of sequence kindly provided by M.Lehrman (22-APR-1987).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lehrman, M.A., Goldstein, J.L., Russell, D.W. and Brown, M.S.
Duplication of seven exons in LDL receptor gene caused by Alu-Alu recombination in a subject with familial hypercholesterolemia Cell 48 (5), 827-835 (1987)
87131094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMLDLRFL 90 bp DNA PRI 11-JAN-19
Human low density lipoprotein receptor intron A Alu repeat.
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Eutheria; Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 90)
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                Unclassified
                                                    Unknown.
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(bases 1 to 60)
                                                                                                                                                                                                                                                                                                       0.1%; Score 39; DB 9; I ilarity 100.0%; Pred. No. 8.2e-08; Conservative 0; Mismatches 0;
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a
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/note="hgml; G00-119-362"
/note="hgml; G00-119-362"
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/db_xref="taxon:9606"
/map="19p13.3"
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8 c 19 g
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HUMBRKFAC/c
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                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 80)

Kornreich, R., Bishop, D.F. and Desnick, R.J.

Alpha-galactosidase A gene rearrangements causing Fabry disease:
Identification of short direct repeats at breakpoints in an
                                                                                                                                                                                                                       Human alpha-galactosidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AR051499 76 bp
Sequence 69 from patent
AR051499
AR051499.1 GI:5974863
                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                  Fabry disease; breakpoint junction; glycosphingolipid Human DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neural thread protein gene expression
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de la Monte, S. and Wands, J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unclassified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unknown.
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Neural thread protein gene expression
                                                                           Alu-rich
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Similarity 100.0%;
38; Conservative 0;
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                                     Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
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19 c 18 g
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14 c 15 g
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2.5e-07;
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   HUMLDLRA2
                                                                                                                                                            38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clean copy of sequence kindly provided by M.Lehrman (22-APR-1987). Individual FH 295 carries two mutant LDL receptor alleles. The allele below was inherited from the and includes a duplication of exons 2 through 8 that was presumably created by unequal chromosomal crossover involving Alu repeats in introns 1 and 8. The exact site of recombination cannot be determined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l (bases 1 to 90)
Lehrman, M.A., Goldstein, J.L., Russell, D.W. and Brown, M.S.
Duplication of seven exons in LDL receptor gene caused by Alurecombination in a subject with familial hypercholesterolemia Cell 48 (5), 827-835 (1987)
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Alu repeat; LDL receptor; cell surface
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Eutheria; Primates; Catarrhini; Hominidae; Homo
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Human (FH 295) fibroblast DNA, clone p295.
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                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                       /note-"LDLR duplicated intron 1 (no splice 68); putative; does not fit consensus" 33 c 19 g 20 t tream of NheI site; chromosome 19p13.2-p13.1
                                                                                                                                                                                                                                                                                                                                     /note="LDLR intron 8; G00-119-362" 43. .68
 97
density
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/db_xref="taxon:9606"
/map="19p13.3"
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2.6e-07;
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2.6e-07;
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PRI
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38; Conserv
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Chromosome 19p13.2-p13.1.
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                                                                                                                                                                                                                                                                                                                                                                                          M14179.1 GI:187101

low density lipoprotein receptor-1; very low density lipoprotein.

Human fibroblast DNA, from patient FH-626.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human
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1 (bases 1 to 97)
                                                                                                              Analysis of the LDL-receptor gene of a patient with familial hypercholesterolemia (PH) revealed the deletion of exon 5 resulting from a homologous recombination between repetitive Alu sequences of
                                                                                                                                                                                                    Hobbs,H.H., Brown,M.S., Goldstein,J.L. and Russell,D.W. Deletion of exon encoding cysteine-rich repeat of low density lipoprotein receptor alters its binding specificity in a subject with familial hypercholesterolemia
J. Biol. Chem. 261, 13114-13120 (1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Analysis of the LDL-receptor gene of a patient with familial hypercholesterolemia (FH) revealed the deletion of exon 5 resulting from a homologous recombination between repetitive Alu sequences of intron 4 and intron 5.
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Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 97)
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familial hypercholesterolemia 626-a gene with a deletion of
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34 c 25 g 19 t
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/db_xref="taxon:9606"
/map="19pl3.3"
/oin(M14178.1:1..97,1..97)
/gene="LDLR"
       /organism="Homo sapiens"
/db_xref="taxon:9606"
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es 37; Conserv
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Chromosome 19p13.2-p13.1.
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     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Cattarrhini; Hominidae; Homo.

1 (bases 1 to 101)

Bernard,O.A., Romana,S.P., Schichman,S.A., Mauchauffe,M.,
Jonveaux,P. and Berger,R.
Partial duplication of HRX in acute leukemia with trisomy 11
                                                                                                                                                                                                                                                                   S79561 101 bp DNA PRI 27-JAN-1996 dHRX [partial genomic duplication startpoint] (human, acute myeloid leukemia with trisomy 11 syndrome patient J, Genomic Mutant, 101
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Eutheria; Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 101)
Bernard, O.A., Romana, S.P., Schichman, S.A., Mauchauffe, M.,
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HRX {intron 6} [human,
$79560
                                                                                                                                          Homo sapiens
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Partial duplication of HRX in acute leukemia with trisomy 11
Leukemia 9 (9), 1487-1490 (1995)
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                                                                                                                                                         human acute myeloid leukemia with trisomy 11 syndrome patient J.
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/db_xref="taxon:9606"
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                                                                                                               Human HepG2 3'
D17279
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Sequence 1 from Patent WO9801573.
A68621
                                      Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
                                                                Homo sapiens
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Resnick, M.A., Larionov, V.L., Kouprina, N.Y. and Perkins, E. TRANSFORMATION ASSOCIATED RECOMBINATION CLONING Patent: WO 9801573-A 15-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unidentified
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Map location: 11q23.
               Matoba, R
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                                                                                                                                                                                                                                                                                                                                                    CCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL MEDLINE
                                                                                                                                                                                                             JOURNAL
28372 ACCTCCGCCTCCCGGGTTCAAGCGATTCTCCTGCCT 28407
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Query Match 0.1%; Score 36; Best Local Similarity 100.0%; Pred. No. Matches 36; Conservative 0; Mismatc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19138 CCACTGCACTCCAGCCTGGGCGACAGAGGCGAGACTC 19173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 CCACTGCACTCCAGCCTGGGCGACAGAGCGAGACTC 43
        l Similarity
36; Conserv
                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 103)

Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.
Alu RNA transcripts in human embryonal carcinoma cells. Model post-transcriptional selection of master sequences
J. Mol. Biol. (1992) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M87896.1 GI:174874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human carcinoma
M87896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 51)
Matoba,R., Okubo,K., Hori,N., Fukushima,A. and Matsubara,K.
Matoba,R., Okubo,K., Hori,N., Fukushima,A. and Matsubara,K.
The addition of 5'-coding information to a 3'-directed cDNA library
improves analysis of gene expression
Gene 146 (2), 199-207 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (21-JUL-1993) to the DDBJ/EMBL/GenBank databases. Ryo Matoba, Osaka University. Institute for Molecular and Cellular Bio: 1-3, Yamada-oka, Suita, Osaka 565, Japan (E-mail:matoba@inherit.imcb.osaka-u.ac.jp, Tel:81-6-877-5111(ex.3314), Fax:81-6-877-1922)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alu repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens male embryo carcinoma cDNA to other RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMALCE221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phone: 07747-5-2308
Fax: 07747-5-2321.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecular Microbiology and Genetics Lab.
Research Institute of Innovative Technology
Rizugawadai Kizu-cyo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (21-Jul-1993) to DDBJ by:
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        Conservative
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/db_xref="taxon:9606"
/cell_line="HepG2"
/clone_lib="Kiseru"
                                                                                                                           /tissue_type="carcinoma"
27 c 33 g 1
                                                                                                                                                                                                                                 /organism-"Homo sapiens"
/db_xref-"taxon:9606"
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19 c
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na cell-derived
    %; Score 36; DB
%; Pred. No. 2.5
0; Mismatches
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                       DB 9; Le
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2.5e-06;
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clone CE221.
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Search completed: March 31, 2000, 06:36:34 Job time: 184343 sec

Page 6

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No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.
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                                                                                                    Template switching
Intronic human MSH
Primer, RI-Not-T30
Primer MBTC from W
                                                                                                                                                                                                                                                                                 Self-complementary
Porcine reproducti
Splint oligonucleo
pV3TA-LTR oligonuc
PR-1 promoter prim
PR-1 promoter prim
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Oligonucleotide 43
Oligonucleotide 43
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                           PCR suppression pr
Primer of the spec
EP-892047 Seq ID 1
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3' portion of cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence of primer Trypsin inhibitory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alu PCR primer 2.
Alu PCR primer 1.
Inter-Alu specific
  cDNA synthesis
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                                                                                                                                                                                                                                                                                                                                                                                                                                            primer AL1. Nu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 1
V19045/c
ID V19045;
AC V19045;
DT 28-JUL-1998 (first entry)
DE Alu PCR primer 2.
KW PCR; primer; amplification;
KW circular yeast artificial (
OS Synthetic.
OS Saccharomyces sp.
PN W09801573-Al.
PD 15-JAN-1998;
PF 09-JUL-1996; WO-U11478.
PR 09-JUL-1996; WO-U11478.
PR (USSH) US DET HEALTH & HI
PI Kouprina NY, Larionov VL, I
DR WF; 98-110234/10.
PT recombination using vector
PT yeast telomere and nucleic
PS Example 1; Page 45; 117pp;
CC This is the nucleotide sequence of DNA is known.
CC the creation and use of ci.
Ct to selectively clone specific sequence of DNA is known.
CC sequence of DNA is known.
                                                                                                                                                                                                                                                                                                               RESULT
V19044
     DA COS SOO DE PN OS SOO DE PN O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Preparation of yeast artificial chromosomes - by in vivo recombination using vector comprising yeast centromere, marker, yeast telomere and nucleic acid for recombination Example 1; Page 45; 117pp; English.

Example 1; Page 45; 117pp; English.

C This is the nucleotide sequence for the PCR primer used in the complification of the Alu repeat sequence, which is used to demonstrate the processes described in the invention. It involves the creation and use of circular yeast artificial chromosome (YAC) to selectively clone specific nucleic acids from a background of mixed nucleic acids by introducing the vector(s) into E. coli cells. They can be used to rapidly isolate human DNA where only a part of the sequence of DNA is known. Using the methods large fragments of DNA can be easily cloned and analysed.

SQ Sequence 40 BP; 9 A; 8 C; 19 G; 4 T;
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Best Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces sp.

W09801573-A1.

15-JAN-1998.

09-JUL-1996; U11478.

09-JUL-1996; WO-U11478.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alu PCR primer 1. PCR; primer; amplification; Alu repeat sequence; vector; circular yeast artificial chromosome; YAC; ss. Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alu PCR primer 2. PCR; primer; amplification; Alu repeat sequence; vector; circular yeast artificial chromosome; YAC; ss.
                                                                                                                                                                                                                                                            V19044 standard; DNA; 40 BP
V19044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JAN-1998.
09-JUL-1996; WO-U11478.
09-JUL-1996; WO-U11478.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
KOUDTINA NY, LATIONOV VL, PERKINS EL, RE
WPI; 98-110234/10.
                                                                                                                                                                                                                                 28-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JUL-1998 (first entry)
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T33764
T98502
T88002
T88002
V24462
V24019
V354966
X19061
V83890
T17031
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
0.032;
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Primer/probe used
cDNA synthesis pri
Primer used in iso
PCR primer for cho
PCR primer for Hum
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Human mitochondria
Knot probe P302 us
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Human PPAR-gamma o
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OM nucleic

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nucleic search, using sw

model

GenCore version 4.5 Copyright (c) 1993 - 2000 Com

WPI; 98-110234/10

USSH) US DEPT HEALTH & HUMAN SERVICES.

Preparation of yeast artificial chromosomes - by in vivo recombination using vector comprising yeast centromere, marker, yeast telemere and nucleic acid for recombination Example 1; Page 45; 117pp; English.

This is the nucleotide sequence for the PCR primer used in the amplification of the Alu repeat sequence, which is used to demonstrate the processes described in the invention. It involves the creation and use of circular yeast artificial chromosome (YAC) to selectively clone specific nucleic acids from a background of mixed nucleic acids by introducing the vector(s) into E. coli cells. They can be used to rapidly isolate human DNA where only a part of the sequence of DNA is known. Using the methods large fragments of DNA can be easily cloned and analysed.

Sequence 40 BP; 7 A; 13 G; 8 T;

Length 40

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RESULT 4
Q77890/c
Q77890 standard; cDNA; 30 BP
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                                                                                                                                                                           Query Match
Best Local
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Best Local
                                                                                                                                                             Matches
                                                                                                      claim 6; Page 6; 31pp; English.

Primer PDJ33 is one of several primers which are preferred for use in amplifying inter-Alu regions of DNA. The amplified fragments are then subjected to 2-D electrophoresis on the basis of length and differences in base sequence. The resulting separation pattern is transferred to a filter for screening with a probe. The method can be used to detect genetic variation.

See 027389-027404 and 033141-033144.

Sequence 35 BP; 8 A; 10 C; 11 G; 6 T;
Neural thread protein ADIO-7 cDNA 5' antisense oligonucleotide
               06-JUL-1995
                                                                                                                                                                                                                                                                                                                                                            Detection of genetic variation by 2-D electrophoresis of fragments - and hybridisation with labelled probes, carried on fragments consisting of inter-repeat sequences generated
                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 92-284683/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                            06-AUG-1992.
24-JAN-1992; NL0018.
25-JAN-1991; NL-000132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polymerase chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77-7AN-1993 (first entry)
Inter-Alu specific primer PDJ33.
Polymerase chain reaction; PCR;
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227391 standard; DNA; 35
                                                                                                                                                                                                                                                                                                                                                                                                                                 (INGE-) INGENY BV.
                                                                                                                                                                        Local
                                                                                                                                                           Similarity
35; Conser
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                                                                                                                                                          0.1%; Silarity 100.0%; I Conservative 0;
              (first entry)
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Pred. No. 0.69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repetitive element;
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                                                                                                                                                             Mismatches
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28388 TTCAAGCGATTCTCCTGCCTCAGCCTCCC 28416

Query Match Best Local S Matches 29

Similarity

100.0%;

DB 1; 27;

Length 30;

0;

Gaps

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Conservative

0 Score 29; Pred. No.

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RESULT 5
1D 727744/s
1D 727744/s
1D 727744/s

AC 727744,
DT 14 NOV-1996 (first entry)
DE Neural thread protein antisens
KW Albeimer's disease; neuroecte
KW Albeimer's disease; neuroecte
KW Albeimer's disease; neuroecte
KW Monoclonal antibody; binding 1
OS Synthetic.
PN W09615272-Al.
PF 14-NOV-1995; U17111.
PF 14-NOV-1995; U2-340426.
PR (ABHO) GEN HOSPITAL CORP.
PR 14-NOV-1994; U3-340426.
PR (ABHO) GEN HOSPITAL CORP.
PI Detection of neural thread profection of neural thread profection of neural thread profection of neural thread profection of containing the profection of machaling the profection of binding to the profection of binding to the profection of binding to the profection of containing the profection of containing the profection of containing the profection of binding tragment of eith CC diagnosing the presence of All CC diagnosing the presence of containing the profection of a binding fragment of eith CC diagnosing the presence of containing the profection of containing the profection of a binding fragment of eith CC diagnosing the presence of actuments and a malianant astron CC (see T27739-44).
Sequence 30 BP; 8 A;
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protection of neural thread protein in diagnosis of Alzheimer's protesses - also NTP DNA and protein sequences used in gene and antisense therapy antisense therapy bisclosure; Page 48; 238pp; English.

A method for detecting the presence of neural thread protein (NTP) A method for detecting the presence of neural thread protein (NTP) having a molecular weight of 8, 14, 17, 21, 26 or 42 kD in a human subject comprises (a) contacting a sample from a human subject that is suspected of containing the NTP with at least one molecule is suspected of containing the NTP with at least one molecule capable of binding to the protein; and (b) detecting any of the molecule bound to the protein. The binding molecule is selected from an antibody free of natural impurities, a monoclonal antibody or a binding fragment of either of these. The method may be used for diagnosing the presence of Alzheimer's disease, neuroectodermal tumours and a malignant astrocytoma in a human. Expression of NTP nucleic acid may be inhibited using antisense oligonucleotides (See T27739-44).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 29
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(GEHO ) GEN HOSPITAL CORP.

DE LA MONTE SM. Wands TP

WPI; 94-341497/42

Detection Of fam' 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28388 TICAAGCGATICTCCTGCCTCAGCCTCCC 28416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detection of neural thread proteins - to detect sporadic and familial Alzheimer's disease, neuroectodermal tumours, malignant astrocytomas and glioblastomas (Eng).
Disclosure: Page 48: 158pp: English.
077888-077890 are ADIO-7 neural thread protein (NTP) antisense oligonucleotides, that can be used to down regulate or inhibit the expression of the NTP gene. These oligonucleotides could be used in the treatment of the folowing conditions Alzheimer's disease, neuroectodermal tumours, malignant astrocytomas and glioblastomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-NOV-1996 (first entry)
Neural thread protein antisonse sequence.
Neural thread protein; NTP; diagnosis; detection;
Alzheimer's disease; neuroectodermal tumour; malignant astrocytoma;
monoclonal antibody; binding fragment; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neural thread protein AD10-7; Alzheimer's; neuroectodermal tumours; malignant astrocytomas; glioblastomas; \mathbf{5}' antisense therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 29; DB 1;
Pred. No. 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 30
                                                                                                                                                     antibody
be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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TTCAAGCGATTCTCCTGCCTCAGCCTCCC

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THE RESULT TO SEE THE 
        TRESULT
T98500/c
ID T985
AC CDNA
KW Temp
KW PCR
KW PCR
Synt
FN W097
PD 10-3-3
PF 03-3-3
PF 03-3-2
PA (CLC
PA (CLC
PA (CLC
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PA (CL
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PS Claim 9; Page 29; 39pp; English.
CC T98497-T98520 represent primers used in the method of the invention. The CC method of the invention is for preparing DNA complementary to the 5'-end CC of an RNA molecule. The method comprises annealing a cDNA synthesis CC primer to the RNA molecule and synthesising a first DNA strand CC complementary to at least a portion of the RNA molecule, and contacting the RNA molecule with a template switching oligonucleotides (TSO) (such as T98426) having a pre-selected nucleotide sequence at its 5'-end and at cC least 1 riboguanine residue at its 3'-end, where the TSO binds the 5'-end cof the RNA molecule and serves as a template for the extension of the CC 3'-end of the first DNA strand. The method can be used for the synthesis and cloning of full length cDNA, or fragments, that correspond to the CC construct cDNA libraries from nanogram quantities of total or poly A+ CC RNA. The TSO allows for negative selection against cDNA that are not complementary to the 5'-end of the template RNA, while allowing full CC length cDNA to be readily selected.

Sequence 55 BP; 10 A; 5 C; 7 G; 33 T;
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Best Local s
Matches 29
                                                                                                                           Synthetic.
W09724455-A2.
10-JUL-1997.
10-JAN-1997: U00368.
03-JAN-1996; US-582562.
(CLON-) CLONTECH LAB INC.
Chenchik A, Diatchenko L,
WPI: 97-363690/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26680 AAAAAAAAAAAAAAAAAAAAAAAAAGTA 26708
Preparation of cDNA from RNA molecules primer to RNA, synthesising DNA and conswitching oligo:nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Template switching oligonucleotide; RNA/DNA hybrid; DNA preparation, cDNA synthesis primer; cDNA cloning; cDNA library construction; PCR primer; amplify; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-MAR-1998 (first entry) cDNA synthesis primer Fr-T30NN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CLON-) CLONTECH LAB INC. Chenchik A, Diatchenko I WPI; 97-363690/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-JUL-1997.
03-JAN-1997; U00368.
03-JAN-1996; US-582562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T98500;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Template switching oligonucleotide; RNA/DNA hybrid; DNA preparation; CDNA synthesis primer; cDNA cloning; cDNA library construction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9724455-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98500 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARABARABARABARABARABARABARABGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        o.1%; s
l similarity 100.0%;
29; Conservative 0;
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                                                                                                                                                                       Siebert P,
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Pred. No. 23;
0; Mismatches
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DNA and conta
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                                            les - by annealing cDNA synthesis contacting with novel template
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contacting with novel
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23;
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28

RESULT

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19152

CCTGGGCGACAGAGCGAGACTCTGTCTC

CCTGGGCGACAGAGCGAGACTCTGTCTC

Query Match
Best Local Similarity
Matches 28; Conser

Conservative

0

Mismatches 19179

0.1%;

Score Pred.

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50; 1; 0

Length 28;

Indels

0,

Gaps

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RESULT 8
T12509/c
ID T12509 standard;
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CC T98497-T98520 represent primers used in the method of the invention. The CC method of the invention is for preparing DNA complementary to the 5'-end CC of an RNA molecule. The method comprises annealing a cDNA synthesis CC complementary to at least a portion of the RNA molecule, and contacting CC complementary to at least a portion of the RNA molecule, and contacting CC as T98426) having a pre-selected nucleotide sequence at its 5'-end and at CC least 1 riboguanine residue at its 3'-end, where the TSO binds the 5'-end CC in the RNA molecule and serves as a template for the extension of the CC in the RNA molecule and serves as a template for the extension of the CC complete sequence of the 5'-end of the method can be used for the synthesis CC complete sequence of the 5'-end of the mana molecule. It can be used to CRA. The TSO allows for negative selection against cDNA that are not CC complementary to the 5'-end of the template RNA, while allowing full CC length cDNA to be readily selected.

Sequence 58 BP; 8 A; 5 C; 9 G; 34 T;
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PT Quantifying genomic DNA by amplification of repetitive sequences - prin presence of internal standard, then comparing amts of amplified genomic DNA and standard, partic. for quality control of recombinant proteins, vaccines, etc.

PS Claim 13; Page 14; 41pp; German.

CC Primers T12508 9 are used to amplify a 146 bp fragment of an Alu repeat sequence in a novel method of quantitating genomic DNA in a sample. The convel method features the addition of a known amount of an internal convel method feature. The template for these primers is the plasmid pAlu-wt which comprises plasmid pCRII contg. nucleotides 148-294 of the Alu repeat sequence given in Nucleic Acid Res., 18 (1990) 6793. The method is esp. useful for the detection of contaminating DNA in the manufacture of therapeutic prods.

SQ Sequence 28 BP; 5 A; 9 C; 9 G; 5 T;
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Best Local
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Kohl J
                                                                                                                                                                                                                                                                                                         WPI; 96-069063/08
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26-SEP-1994; AT-001830.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   quantitation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primer Alu B
Primer; PCR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-SEP-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
corresp. to bases 294-267.
polymerase chain reaction; amplification; Alu repeat; ss;
pinternal standard; plasmid; contamination; therapeutic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA;
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Pred. No. 22;
0; Mismatches
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misc_difference Homo sapiens.

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RESULT 10
Q73570/c
Q73570/c
ID Q73570 standard; DNA; 32 BP.
AC Q73570,
DT 25-UTW-1995 (first entry)
DE Enhancer element er-3 conserved basepair sequence.
KW Enhancer element; carcinoma; tumor; cancer; SLPI gen
KW secretory leukoprotease-inhibitor gene; cyrokeratin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-SEP-1994; U03197.
Fr 24-MAR-1994; U03197.
Pr 24-MAR-1993; US-035435.
A (UABR-) UAB RES FOUND.
Garver Rr, Sorscher EJ;
DA construct for treating human carcinoma - includes a
DA construct for treating human carcinoma - includes a
DA construct for treating human carcinoma - includes a
DA construct for treating human carcinoma - includes a
DA construct for treating human carcinoma sequences
This enhancer sequence is part of a DNA construct used for treating human carcinoma which contains a cancer therapeutic protein under the control of a promoter and 3 enhancer sequences in a specific 5'-3'
Corder. This enhancer element is derived from the flanking region of the human epithelial cell cytokeratin-8 gene.
Sequence 32 BP; 7 A; 1 C; 8 G; 15 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28461 ATTTTTGTATTTTTAGTAGAGATGGGGT 28488
                           Garver RI) Sorscher EJ;

WRI; 94-316537/39.

DNA construct for treating human carcinoma - includes a cancer-therapeutic gene under the control of a promoter and a gp. of enhancer sequences claim 1; Fig.6; 54pp; English.

This enhancer element is part of a DNA construct used for treating human carcinoma which contains a cancer therapeutic protein under the control of a promoter and 3 enhancer sequences in a specific 5'-3' order. This enhancer element is derived from the flanking region of the human epithelial cell cytokeratin-8 gene.

Sequence 32 BP; 7 A; 1 C; 8 G; 15 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             secretory leukoprotease-inhibitor gene; cytokeratin gene-8;
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Similarity 100.0%;
28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         US-035435.
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/label=
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pyrimidine
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         μ.
11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene;
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205168/c
ID 06517
AC 0551
DT 2551
PN 0605
PA (CO'
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PA (MOCH) MOCHIDA PHARM CO LTD.

RWPI; 95-35285/46.

RWPI; 95-35285/46.

PO WPI; 95-35285/46.

PO MOCHIDA PHARM CO LTD.

PO WPI; 95-35285/46.

PO A polypeptide having trypsin inhibitory activity - for the treatment profile for the profile for trypsin inhibitory activity, mol.wt. 22-28 kD and polypeptide having trypsin inhibitory activity, mol.wt. 22-28 kD and polypeptide having trypsin inhibitory activity, mol.wt. 22-28 kD and polypeptide having trypsin inhibitory activity, mol.wt. 22-28 kD and polypeptide was isolated from human T98G and is useful for treathing bancreattitis, shock, multiple organ failure and disseminated intravascular coagulation. The present sequence is that of an antisense primer used for cloning T98G CDNA coding for the full-length polypeptide.

Sequence 48 BP; 2 A; 1 C; 1 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 28
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Best Local
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24-JUN-1992; US-903421.
(CORR) CORNELL RES FOUND INC.
(UVNY) UNIV NEW YORK MT SINAI.
SCHOOL MEDICINE.
GELMAN IH, LAURENCE JC;
WPJ: 94-026200/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
J07242700-A.
19-SEP-1995.
04-MAR-1994;
04-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-JAN-1994.
23-JUN-1993;
24-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4696 AAAAAAAAAAAAAAAAAAAAAAAAAAA 4723
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HIV-LP useful in vaccine formulations - is novel HIV virus distinct from HIV-1 and or HIV-2 viruses

Example; page 7; 75pp; English.

HIV-LP is a new variant of the HIV family. A cDNA first strand synthesised from Pt. 1 pellet using MLV RT. The product was converted into dsDNA and this cDNA was amplified by PCR using primers 055167 and 055168.

Sequence 40 BP; 3 A; 2 C; 3 G; 32 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-MAY-1996 (first entry)
Trypsin inhibitory protein cDNA antisense primer-1.
Trypsin inhibitor, human T98G cells; pancreatitis; shock; DIC;
Trypsin; inhibitor, human T98G cells; pancreatitis; shock; DIC;
multiple organ failure; disseminated intravascular coagulation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
WO9400562-A.
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Sequence of primer for PCR amplification of HIV-LP Pt.1 isolate
Human immunodeficiency virus; HIV-LP; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q55168 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04081 standard; DNA; 48 BP
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JP-059906
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Pred. No.
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. 49;
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Query Match Best Local

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24-MAR-1993;

WO9421118-A. 29-SEP-1994. 24-MAR-1994; U03197

misc_difference

Homo sapiens.

(UABR-) UAB RES FOUND Garver RI, Sorscher 1

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RESULT
T88080
ID TE
AC TE
DT 14
DE 3'
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                                                                                                                                                                                                                                                                           PT regulating, immunomodulating and many other activities are S lisclosure; Page 86; 139pp; English.

CC The present sequence encodes a portion of a novel human secreted protein can be compared under accession number ATCC 98026. The secreted protein can be used to determine biological activity, to raise antibodies, as tissue that modulate their interactions and as nutritional supplements. It may called have a very wide range of biological activities although no conviction of other cytokines; immunostimulating activity or calculation of other cytokines; immunostimulating/immunosuppressant cantivities (e.g. for treating human immunodeficiency virus infection, concer, autoimmune diseases and allergy); regulation of haematopoiesis (e.g. for treating anaemia or as adjunct to chemotherapy); stimulation treating mounds, periodontal disease, neurological diseases stroke, concer, autoimmune disease, neurological diseases stroke, concerning the control of fertility); chemotactic and chemotherapy; stimulation of fibrosis; inhibition or stimulation of follicle stimulating hormone control of fertility); chemotactic and chemokinetic activities (e.g. for treating infections, tumours); haemostatic or thrombolytic activity (e.g. for treating septic shock, Crohn's cativity (e.g. for treating septic shock, Crohn's as antimicrobials; for treating sportasis or other hyperproliferative disease; for regulation of metabolism, behaviour, and cardid in gene therapy procedures.

Sequence 49 BP; 40 A; 2 C; 6 G; 1 T;
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Best Local S
Matches 28
                                                                                                                                    T88080;
14-MAY-1998 (first entry)
3' portion of cDNA clone encoding secreted
                                                       T88080 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New secreted proteins encoded clones present in ATCC 98026 - possibly having cytokine, cell proliferation/differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spaulding V;
WPI; 97-526460/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GEMY ) GENETICS INST INC.
Jacobs K, Lavallie ER, McCoy JM, Merberg D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-APR-1997; U06139.
18-APR-1996; US-634325.
(GEMY) GENETICS INST I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human secreted protein AK533 3' portion including the polyA tail Human; secreted protein; ATCC 98026; cytokine; immunomodulation; cell proliferation; differentiation; regulation; ds.
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                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                         larity 100.0%;
Conservative (
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ilarity 100.0%;
Conservative (
                                                     CDNA; 49 BP.
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                                                                                                                                                                                                                       Score 28;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 28; DB; Pred. No. 43; 0; Mismatches
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                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                       43;
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43;
 Protein AK533
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                                                                                                                                                                                                                                    Length 49
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C inhibition activitles. It can also be used to research or treat diseases/disorders related to its function.

The partial cDNA clone AP162 was 1st isolated from a human adult placenta cDNA library. The partial cDNA clones AM931, AM610, AM340, AM610, AK633, AK633, AM633, AK633 and AK296 were 1st isolated from a human cross feetal kidney cDNA library. The partial cDNA clones H617 and BB9 were 1st isolated from a human peripheral blood monocyte cell (Th1 Crom a human ovary (PA-1 teratocarcinoma) cDNA library. The partial cDNA clone AW191 was 1st isolated from a human ovary (PA-1 teratocarcinoma) cDNA library. The partial cDNA clones AW210, AM205 and AM310 were 1st isolated from a human foetal broad clones are library. The partial cDNA clones AW211, AM205 and AM319 were 1st isolated from a human foetal brain cDNA clones acount retina cDNA clones AW260 was 1st isolated from a human foetal brain cDNA clones acount retina cDNA clones AR260 was 1st isolated from a human cDNA clones AW201, CNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 28
                                                                               W09837241-A1.
27-AUG-1998.
23-FEB-1998; U03725.
18-JUN-1997; US-050109.
24-FEB-1997; US-038798.
(TMTE-) TM TECHNOLOGIES I
Benight AS, Faldasz BD, L
WPI; 98-467588/40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26678 GGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 26705
                Detecting telomerase activity - without the need for polymerase chain reaction amplification, can be adapted to assay for telome inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                18-NOV-1998 (first entry)
DNA detector sequence used in a telomeric activity assay.
Telomerase; telomeric repeat sequence; carcinogen; seneso
                                                                                                                                                                                                                                                                                                                                   misc_binding
                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
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V54636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human and murine secreted proteins - useful to research or treat diseases or disorders related to their function Disclosure; Page 86; 140pp; English.
The present sequence is the 3' portion of a cDNA clone encoding a human secreted protein, which may have nutritional uses, or cytokine and cell proliferation/differentiation, immune stimulating or suppressing, haematopolesis regulating, tissue growth, activin/inhibin, chemotactic/chemokinetic, haemostatic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Theoharides TC;
WPI; 97-526459/48.
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11-APR-1997; U06042.
12-APR-1996; US-631184.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 100.
28; Conservative
  Fig 1C;
                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers 31. .54
                                                                                                                                                                                                                                                   /*tag= a
/note= "Forms a double-stranded region
bases 38-60 of V54639"
9pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.1%;
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                                                                                                       INC.
English
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43;
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                                                                                                                                                                                                                                                                                                                                                                                                                senescence;
                                for telomerase
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The invention provides a method for detecting the presence of telomerase cc activity. The method comprises of (a) providing a test nucleic acid, ce .g. the nucleic acid sequence shown in V54635, that will be elongated cc by telomerase; (b) incubating the test nucleic acid with the sample cc nucleic acid, e.g. see V54639, using a detecting the elongated cc nucleic acid, e.g. see V54639, using a detector sequence such as the cc immobilised on a solid support, comprises of a hairpin and/or a felomeric repeat sequence, prior to elongation by telomerase. Detection cc of telomeric repeat sequence, prior to elongation by telomerase. Detection cc carcinogenicity and senescence in cells. The assay is also claimed to be useful for determining the effects of compounds on telomerase activity is claimed to be useful for determining the effects of compounds on telomerase carcinogenicity and senescence in cells. The assay is also claimed to the treatment of cancers.

So sequence 53 BP; 7 A; 12 C; 1 G; 33 T;
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Query Match 0.1%; Score 28; DB 1; Length 53; Best Local Similarity 100.0%; Pred. No. 42; Matches 28; Conservative 0; Mismatches 0; Indels

0; Gaps 0; ...

Search completed: March 31, 2000, 10:14:26 Job time: 195864 sec

Page 6

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Minimum DB
Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Result
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
   length: 8 length: 105
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Match
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10565.402 Million cell updates/sec
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     GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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/cgn2_6/ptodata/1/ina/5D_COMB.seq:*
/cgn2_6/ptodata/1/ina/6_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-08-450-573C-69

US-08-450-673C-69

US-08-450-673C-69

US-08-450-673C-69

US-08-450-673C-69

US-08-778-494B-67

US-08-778-494B-109

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US-08-778-494B-109

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US-08-450-673C-91

US-08-450-673C-91

US-08-450-673C-91

US-08-450-673C-91

US-08-450-673C-91

US-08-233-609-5

US-08-233-609-5

US-08-233-609-5

US-08-243-129-5

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                                                                                   Query Match
Best Local Similarity
                                                                    Matches
                                     9496 GCTAATTTTTGTATTTTTAGTAGAGACAGGGTTTCACC 9533
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     Conservative
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27 28 0.1 60 3 US-08-454-557C-58 Sequence 58, Appl 28 0.1 60 4 US-08-340-426D-58 Sequence 58, Appl 39 28 0.1 60 4 US-08-340-426D-58 Sequence 58, Appl 28 0.1 60 4 US-08-340-426D-58 Sequence 58, Appl 31 28 0.1 60 4 US-08-450-673C-58 Sequence 58, Appl 32 28 0.1 60 6 PCT-US95-17111A-58 Sequence 58, Appl 39 28 0.1 78 3 US-08-454-557C-70 Sequence 70, Appl 37 28 0.1 78 3 US-08-454-557C-70 Sequence 70, Appl 39 28 0.1 78 4 US-08-340-426D-70 Sequence 70, Appl 39 28 0.1 78 4 US-08-340-426D-70 Sequence 70, Appl 40 28 0.1 78 4 US-08-450-673C-70 Sequence 70, Appl 40 28 0.1 78 4 US-08-450-673C-70 Sequence 70, Appl 40 28 0.1 78 4 US-08-450-673C-70 Sequence 70, Appl 40 28 0.1 78 4 US-08-450-673C-70 Sequence 70, Appl 40 28 0.1 78 4 US-08-450-673C-70 Sequence 70, Appl 40 28 0.1 78 6 PCT-US95-17111A-70 Sequence 70, Appl 40 28 0.1 78 6 PCT-US95-17111A-70 Sequence 70, Appl 40 28 0.1 78 6 PCT-US95-17111A-70 Sequence 70, Appl 40 28 0.1 78 6 PCT-US95-17111A-70 Sequence 70, Appl 40 28 0.1 78 6 PCT-US95-17111A-70 Sequence 70, Appl 40 28 0.1 78 6 PCT-US95-17111A-70 Sequence 70, Appl 40 28 0.1 78 6 PCT-US95-17111A-70 Sequence 70, Appl 40 28 0.1 78 6 PCT-US95-17111A-70 Sequence 70, Appl 40 28 0.1 78 6 PCT-US95-17111A-70 Sequence 70, Appl 547846-1	O	ი		ი		o		O		ი		Ω Ω		ი		ი		ი	
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50 3 US-08-454-557C-58 Sequence 58, 560 4 US-08-340-426D-58 Sequence 58, 60 4 US-08-340-426D-58 Sequence 58, 60 4 US-08-340-426D-58 Sequence 58, 60 4 US-08-450-673C-58 Sequence 58, 60 4 US-08-450-673C-58 Sequence 58, 60 6 PCT-US95-17111A-58 Sequence 58, 60 6 PCT-US95-17111A-58 Sequence 70, 78 3 US-08-454-557C-70 Sequence 70, 78 4 US-08-340-426D-70 Sequence 70, 78 4 US-08-340-426D-70 Sequence 70, 78 4 US-08-340-673C-70 Sequence 70, 78 4 US-08-450-673C-70 Sequence 70, 78 4 US-08-450-673C-70 Sequence 70, 78 6 PCT-US95-17111A-70 Sequence 70, 78 6 PCT-US95-17111A-7	27	27	27	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28	28
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	2,	'n	•	70,	70,	70,	70,	70,	70,	70,	70,	58,	58,	58,	58,	58,	58,	58,	58,

ALIGNMENTS

Sequence 57, Application US/08454557C Patent No. 5830670 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/454,557C FILING DATE: 30-MAY-1995 CLASSIFICATION: 514 ATTORNEY/AGENT INFORMATION: NAME: LUGWIJ, Steven R. REGISTRATION NUMBER: 36,203 REGISTRATION NUMBER: 36,203 GENERAL INFORMATION: APPLICANT: de la Monte, Suzanne APPLICANT: Wands, Jack R. TITLE OF INVENTION: Neural Thread Protein Gene TITLE OF INVENTION: of Alzheimer's Disease TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 371-2600 NUMBER OF SEQUENCES: 1 LENGTH: 60 base pa TYPE: nucleic acid STRANDEDNESS: both COUNTRY: U.S.A. ZIP: 20005-3934 CITY: Washington STATE: D.C. E: Sterne, Kessler, Goldstein & 1100 New York Avenue, Suite 600 60 base pairs both Fox P.L.L.C # Expression and Detection

0.1%;

Score 38; DB; Pred. No. 0.0

0.0042; 0;

Indels

0

0

Length 60;

48

0;

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RESULT 2
US-08-340-426D-57
; Sequence 57, Application US/08340426;
; Patent No. 5948634
; GENERAL INFORMATION:
; APPLICANT: de la Monte, Suzanne
; APPLICANT: Wands, Jack R.
APPLICANT: Wands, Jack R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-340-426D-57
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US-08-450-673C-57
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COMPUTER READLABLE FORM:

COMPUTER READLABLE FORM:

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFFWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/340,426D

FILING DATE: 14-NOV-1994

CLASSIFICATION: 435

CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 0.1%; Score 38; DB 4; Length 60; Best Local Similarity 100.0%; Pred. No. 0.0042; Matches 38; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 5948888
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 57, Application US/08450673C Patent No. 5948888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 60 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9496 GCTAATTTTTGTATTTTTAGTAGAGACAGGGTTTCACC 9533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: LIVE CITY: Washington STATE: D.C.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease UNBER OF SEQUENCES: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A. ZIP: 20005-3934
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                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                       20005-3934
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                                                                                                                                                                                                       Sterne, Kessler, Goldstein & Fox P.L.L.C. 1100 New York Avenue, Suite 600
                                                                                                                      U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
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PCT-US95-17111A-57
; Sequence 57, Application PC/TUS9517111A
; GENERAL INFORMATION:
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US-08-450-673C-57
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Best Local Similarity
Matches 38; Conserv
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NAME: Ludwig, Steven h.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 12021 371-2600
                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340
FILING DATE: 14 NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
                                                                                                                                                             TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LING DATE: 30-MAX-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Storm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9496 GCTAATTTTTGTATTTTTAGTAGAGACAGGGTTTCACC 9533
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SOETWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,673C
FILING DATE: 30-MAX-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPAtible
COMPUTER: IBM FC COMPATIBLE
COMPATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Neural Thread Protein Gene Expression and TITLE OF INVENTION: Detection of Alzheimer's Disease NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, Suite 600
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ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                            STRANDEDNESS:
                                                                                                                                        ENGTH:
                                                                                nucleic acid
nucleic acid
EDNESS: both
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100.0%; Pred. No. 0.004;
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US-08-454-557C-69; Sequence 69, App.; Patent No. 5830
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US-08-340-426D-69
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                                                                             Sequence 69, Application US/08340426D Patent No. 5948634 GENERAL INFORMATION:
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Best Local
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: (SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                           9496 GCTAATTTTTGTATTTTTAGTAGAGACAGGGTTTCACC 9533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/454,557C FILING DATE: 30-MAY-1995 CLASSIFICATION: 514
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APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: de la Monte, S
APPLICANT: Wands, Jack R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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ZIP: 20005-3934
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                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                            18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9, Application US/08454557C
5830670
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                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                  76 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Sterne, Kessler, Goldstein & Fox P.L.L.C. 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                      poth
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100.0%; Pr
.,... 0;
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100.0%; Pred. No.
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0.0042;
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0.004;
                                                                                                                                                                                                                                                                                   Length 76;
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US-08-450-673C-69
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/340,426D
FILING DATE: 14-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 69, Application US/08450673C Patent No. 5948888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,673C
FILING DATE: 30-MAY-1995
CILCUTTERSTON: 530-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 06:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
                                                                                                             CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9496 GCTAATTTTTGTATTTTAGTAGAGACAGGGTTTCACC 9533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Neural Thread Protein Gene Expression TITLE OF INVENTION: of Alzheimer's Disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 38; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A. ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Ludwig, Steven R. REGISTRATION NUMBER: 36,203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                              ZIP: 20005-3934
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ork Avenue, Suite 600
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Pred. No.
                                                            0609.3840004
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                                                                                                                                                                                                                 Version
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TOPOLOGY:
US-08-450-673C-69
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SEQUENCE CHARACTERISTICS:
SEQUENCE TO base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 69, Application PC/TUS9517111A
GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: de la Monte, Suzanne
APPLICANT: wands, Jack R.
APPLICANT: WEUTAL Thread Protein Gene Expression and
TITLE OF INVENTION: Neural Thread Protein Gene Expression and
TITLE OF INVENTION: Detection of Alzheimer's Disease
TUTLE OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                       NAME: Ludwig, Steven R. 203
REGISTRATION NUMBER: 36.203
REFERENCE_DOCKET NUMBER: 0609.3840002
REFERENCE_DOCKET NUMBER: 0609.3840002
REFERENCE_DOCKET NUMBER: 069.3912.9600
TELEPHONE: (202) 371.25400
TELEPAX: (202) 371.2540
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 76 base pairs
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US-08-454-557C-6/c
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COUNTRY: U.S.A.
ZIE: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
COMPUTER: BM PC compatible
COMPUTER: BM PC compatible
SOFTMARE: PATENTION DATA:
SOFTMARE: PAPLICATION DATA:
APPLICATION NUMBER: PCT/US95/17111A
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 08/3/
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
                                                                  STREET: 1100 New CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: both
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Sequence 6, Application US/08454557C Patent No. 5830670
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STATE: D.C.
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: POSP/MS-DOS
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-57C
APPLICATION NUMBER: US/08/454,557C
EILING DATE: 30-MAY-1995
CLASSIFICATION: 514
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (202) 371-2540
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pair
TYPP:
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US-08-340-426D-6/C
US-08-340-426D-6/C
; Sequence 6, Application US/08340426D
; Setent No. 5948544
; GEMERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 0.1%; Score 29; DB 3; Best Local Similarity 100.0%; Pred. No. 2.5; Matches 29; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: TUGWIG, Steven R.

NAME: TUGWIG, Steven R.

REGISTRATION NUMBER: 06
REFERENCE/DOCKET NUMBER: 06
REFERENCE/ION INFORMATION:
TELECOMMUNICATION INFORMATION
TELECOMMUNICATION 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NDDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. 97REET: 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                  NERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, K
AIP: 20005-33-4
ROUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC COMPOSTIBLE
COMPUTER: BM PC COMPOSTIBLE
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
SOPTWARE: Patentin DATA:
US/08/340,426D
                                                                                                                                                                      STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
                                                                                                                                                                                                                            ITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
EDNESS: both
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Wands, Jack R.
                                                                                                                                                                                                                                                       E: Sterne, Kessler, Goldstein & Fox P.L.L.C.
1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION:
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6:
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US-08-340-426D-6
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Best Local Similarity 100.0%;
Matches 29; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                     ATTONNEY AGENT INFORMATION:
ATTONNEY AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609
TELECOMMUNICATION INFORMATION:
TOTAL STATEMENT OF THE S
Ouery Match 0.1%;
Best Local Similarity 100.0%;
Matches 29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -08-450-673C-6/c
Sequence 6, Applica
Patent No. 5948888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28388 TTCAAGCGATTCTCCTGCCTCAGCCTCCC 28416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIDIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1100
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 TICAAGCGATICICCTGCCTCAGCCTCCC 2
                                                                                                                                                                                                                            LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
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STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/450,673C FILING DATE: 30-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORM
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20005-3934
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Ludwig, Steven R.
ATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1100 New York Avenue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATION:
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                               Score 29;
Pred. No.
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   Mismatches
                               DB 4;
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                                                                   Length 30;
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   Indels
0;
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US-08-778-494B-67/c
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                                                                                                                                                                                       Sequence 67, Applicat Patent No. 5962272 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.1%; Score 29; Best Local Similarity 100.0%; Pred. No. Matches 29; Conservative 0; Mismatc
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COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC COMpatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATENTING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                    APPLICANT: Chenchik, Alex
APPLICANT: Zhu, York
APPLICANT: Diachenko, Luda
APPLICANT: Siebert, Paul
TITLE OF INVENTION: METHODS AN
TITLE OF INVENTION: CLONING
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                               28388 TTCAAGCGATTCTCCTGCCTCAGCCTCCC 28416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1100
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Rel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
                                                                                                                                                                                                                                                                                                                         30 TICAAGCGATICTCCTGCCTCAGCCTCCC 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Ludwig, Steve REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/:
FILING DATE: 14-NOV-199:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE
                                                                                                                                                                                                              67, Application US/08778494B
o. 5962272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application PC/TUS9517111A
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1100 New York Avenue, Suite 600
2: Saliwanchik, Lloyd & Saliwanchik
2421 N.W. 41st Street, Suite A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Steven
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                                                                                              AND COMPOSITIONS FOR FULL-LENGTH CDNA
                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 30
                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                     0
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COUNTRY:

USA

Gainesville Florida

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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

CURRENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR FULL-LENGTH CDNA TITLE OF INVENTION: CLONING MUMBER OF SEQUENCES: 114
                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentID Release #1.0
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US 08/582,562
FILING DATE: 03-JAN-1996
CLASSIFICATION: 435
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 08/582,562
APPLICATION NUMBER: 03-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 ААААААААААААААААААААААААА
                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/08778494B
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                                                                                           03-JAN-1997
03-JAN-1997
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                                                                                                                                                                                                   Release #1.0, Version #1.30
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Pred. No. 2.1;
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US-08-454-557C-91/c
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Sequence 91, ...
; Patent No. 583067
; Patent No. 583067
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                     TOPOLOGY: US-08-454-557C-91
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TELECOMMUNICATION INFORMATION:
                                                                                                          Query Match
Best Local Similarity
Matches 29; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
CMEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (202) 371-25
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,557C
APPLICATION NUMBER: 30-MAY-1995
FILING DATE: 30-MAY-1995
                                                               24038 TGTAATCCCAGCACTTTGGGAGGCTGAGG 24066
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REGISTRATION NUMBER: 38,261
                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
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STRANDEDNESS: single
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29; Conserv
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llarity 100.0%;
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e, Suite 600
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TOPOLOGY: 11

MOLECULE TYPE:
US-08-778-494B-67

TELEFAX: (352) 372-5800 INFORMATION FOR SEQ ID NO: 67:

SEQUENCE CHARACTERISTICS: LENGTH: 55 bases

TYPE: nucleic acid STRANDEDNESS: single

linear

NAME: Pace, Doran R.
REGISTRATION NUMBER: 38,261
REFERENCE/DOCKET NUMBER: CLREFERENCE/DOCKET NUMBER: CLTELEPHONE: (352) 375-8100

ATTORNEY/AGENT INFORMATION:

APPLICATION NUMBER: US/OFILING DATE: 03-JAN-1997

Query Match Best Local

0.1%; 1 Similarity 100.0%; 29; Conservative

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US-08-778-494B-109/C

Patent No. 59027
Patent No. 59027
Chenck Sequence 109, App Sequence 109, App Sequence 109, App

Chenchik, Alex

CORRESPONDENCE ADDRESS

APPLICATION NUMBER:

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Search completed: March 31, 2000, 10:04:17 Job time: 195319 sec

Page 7

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ACCESSION
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 97)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
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        Unpublished (1995)
On May 9, 1995 this
Contact: Wilson RK
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The WashU-Merck EST Project
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clone IMAGE:260030 5
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EST 14-FEB-1996
placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA
5' similar to contains Alu repetitive element;,
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AI752407
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A1752407 cn15d10.y
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AA745546 ny56g01.s
AA654896 nt61b07.s
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AA6548738 CIT-HSP-202
A1206968 qr30g11.x
A124836 qr22a66.x
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AA729064 nw22f09.s
AA578401 nl53c01.s
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A1832832 at72g09.x
AQ196366 RPCIII-48
AA988425 cq95q12.s
D20989 HUMGS01971
T62173 y1946212.r1
R7073 y1946212.r1
A1914818 tr25c03.x
AA745546 ny56g01.s
AA515337 ng71c01.s
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N80946 Z812802.r1
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D11650 HUMODDD12
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Matches 45
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        source
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                                                                                                                                                                                                                                                                                                                                  CACCACTGCACTCCAGCCTGGGCGACAGAGCGAGACTCTGTCTCA
                                                                                                                                                                                                                                                     102 bp DN CIT-HSP-669F15.TP CIT-HSP genomic survey sequence. B62983
                                                                Calfrech Genome Research Lab
California Institute of Technology
Division of Biology, MS 147-75; Pasadena, CA
Tel: 626 796 7066
Fax: 626 395 4901
Email: ungdash.tree.caltech.edu
Clones are available from Research Genetics (
                                                                                                                                                                Eukaryota; Metazoa; Chordata; Crania: Eutheria; Primates; Catarrhini; Homin 1 (bases 1 to 102)

Kim, U.-J., Adams, M.D. and Simon, M.I. Determination of clone end sequences
                                                                                                                                                                                                                                                                                                                                                                        45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Putative full_length read
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax:
                                        end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                            Seq primer: SP6
Class: BAC ends.
                                                                                                                                      Unpublished (1997)
Contact: Ung-Jin Kim
                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                            double-stranded CDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT773 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo."

22 c 32 g 20 t
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1. .102
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Location/Qualifiers
                                                                                                                                                                                                                                               GI:2636892
/organism="Homo sapiens'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="GDB:3889736"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Homo
                                                                                                                                                                                                                                                                                                                                                                                 0.1%;
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Pred. No.
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hes 0;
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                                                                                                                                                                  human
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                                                                   (info@resgen.com). BAC
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AUTHORS
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Query Match
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Matches 43
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Best Local Similarity
Matches 45; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 102)
Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. Venter, J.C.
Use of BAC End Sequences for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RPCI11-4N6.TP RPCI-11 Homo
L Similarity
43; Conserv
                                                                                                                                                                                                                                                                                                                                                                               Email: mdadams@tigr.org
Clones are derived from the human BAC library RFCI-11. For BAC
Clones are derived from the human BAC library RFCI-11. For BAC
Clones are derived from the human BAC library RFCI-11. For BAC
Clones may be purchased from
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
(pieter@dejong.med.buffalo.edu). or from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (lift@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
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B48088.1 GI:2600325
                                                                                                                                                                                                                                                                                                                                               Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
Other_GSSs: RPCI11-4N6.TV
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0.1%; Score 43; DB 81; llarity 100.0%; Pred. No. 0.0038; Conservative 0; Mismatches 0
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                                                                                                         /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
24 c 25 g 21 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
/clone="669F15"
/clone_lib="CIT-HSP"
                                                                                                                                                                                         /sex="Male"
                                                                                                                                                                                                           /clone_lib="RPCI-11"
                                                                                                                                                                                                                               /db_xref="taxon:9606"
/clone="RPCI-11-4N6"
                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="GDB:7501469"
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Male"
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sequence.
T52775
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oe02g07.s1 NCI_CGAP_Ov2
similar to contains Alu
AA873656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                       ya79d08.r1 Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:67887 5' similar to contains Alu repetitive element, mRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tumor Gene Index
Unpublished (1997)
On May 8, 1995 this sequence version replaced g1:801221
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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1 (bases 1 to 61)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Insert Length: 553
                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rt Length: 553 Std Error: 0.00 primer: -40ml3 fwd. ET from Amer: quality sequence stop: 51.
                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                           /note-"Vector: pamp10; mRNA made from invasive ovarian tumor, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="NCI_CGAP_Ov2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:1384764"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="ovary"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
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Matches 41
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                                                                                                                       v nv77f06.rl NCI_CGAP_Br4 h
similar to contains Alu r
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EST.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Cr
Eutheria; Primates; Catarrhini;
1 (bases 1 to 72)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High qality sequence stops: 82 Source: IMAGE Consortium, LLNL Thiclone is available royalty-free through LLNL; contact the IMAGE Consortium (infosimage.llnl.gov) for further information. Insert Length: 1013 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
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                                                                                                                   AA715942.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Wilson RK
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"Organ: ovary; Vector: Bluescript SK; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT. Total ovary tissue, normal, caucasian. Average insert size: 0.8 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCACGAG 3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="49 year old"
/lab_host="SOLR cells (kanamycin resistant)"
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/db_xref="GDB:504144"
/db_xref="taxon:9606"
/clone="IMAGE:67887"
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                       Craniata; Vertebrata; Mammalia; i; Hominidae; Homo.
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     Washington University School of Medicine
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AUTHORS
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Best Local Similarity
Matches 40; Conserv
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                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 105)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Hillier,L., Lennon,G., Bubuque,T., Favello,A., Gish,W.,
Chissoe,S., Dietrich,N., DuBuque,T., Ley,M., Le,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
Hawkins,M., Moore,B., Mortis,M., Parsons,J., Prange,C., Rifkin,L.,
Mardis,E., Moore,B., Mortis,M., Soares,M.B., Tan,F., Thierry-Meg,J.,
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J.,
Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T63772 105 bp mRNA EST 17-FEB-1999 yc21f01.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:81337 3' similar to contains Alu repetitive element; r
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumor Gene Index Unpublished (1997)
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                                              Generation and analysis of 280,000 human Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute, Cancer Genome Anat
Contact: Wilson RK
                                                                                                        and Marra, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               primer: -28m13 rev1 ET from h quality sequence stop: 59.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Organ: breast; Vector: pAMP10; mRNA made from normal breast ductal tissue, cDNA made by oligo-dT priming. Non-directionally cloned. Size-selected on agarose gel, average insert size 600 bp. Reference: Krizman et al. (1996) Cancer Research 56:5380-5383."

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/db_xref="taxon:9606"
/clone="IMAGE:1235843"
/clone_lib="NCI_CGAP_Br4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:667637
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/lab_host="DH10B"
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100.0%; Pred. No.
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. Emmert-Buck,
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Insert Length: 451 Std Error: 0.00 Seg primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 50.
                                                                                                                                                         cDNA Library Preparation: David B. Krizman, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: WCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                         On Jan 17, 1998 this sequence version replaced gi:1900439 Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
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1 (Dases 1 to 97)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 513
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//lab_host="SOLR cells (kanamycin resistant)"
//lab_host="SOLR cells (kanamycin resistant)"
//note="Organ: lung; Vector: pBluescript SK-; Site_1:
//note="Organ: lung; Vector: pBluescript SK-; Site_1:
//note="Collaboration of the collaboration of the collaborat
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/clone="IMAGE:81337"
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST 07-APR-1998 sapiens cDNA clone IMAGE:1385090 PTR5 repetitive element ;, mRNA
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734 GAGAATCACTTGAACCTGGGAGGCAGAGGTTGCAGTGAG 772
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                                                                                                                                                                                                                                                                                                                                                                            Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1998)
Other_GSSs: CIT-HSP-2042J24.TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.
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CIT-HSP-2042J24.TR CIT-HSP
genomic survey sequence.
B80126
                                                                                                                                                                                                                                                Seq primer: Mi3 Reverse
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                     Email: mdadams@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of a random BAC End Sequence Database for Sequence-Ready Map
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                              http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
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                                                                                                                        /organism="Homo sapiens"
/db_xref="GDB:7053555"
/db_xref="taxon:9606"
/clone="2042J24"
                                                                                  /sex="Male"
                                                                                                      /clone_lib="CIT-HSP"
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/clone="IMAGE:1385090"
                                       /note="Vector: pBeloBAC11; Site_1:
                                                             /cell_type="Sperm"
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                                                   Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Primates; Catarrhini; Hominidae; Homo.
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Construction of a normalized directionally cloned cDNA library adult heart and analysis of 3040 clones by partial sequencing genomics 35 (1), 231-235 (1996)
1 (bases 1 to 80)
Lanfranchi,G., Muraro,T., Caldara,F., Pacchioni,B., Pallav Pandolfo,D., Toppo,S., Trevisan,S., Scarso,S. and Valle,G. Identification of 4370 expressed sequence tags from a
                                                                                                                                                              HSPD10834 HM3
F24490
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Fax: 81-3-5449-5433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 104)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         University of Tokyo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Yusuke Nakamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tanaka, T., Ogiwara, A., Uchiyama, I., Takagi, T., Yazaki, Y.
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Human heart cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             yusuke@ims.u-tokyo.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                         /Clone="3NHC4544"
/Clone=11b="Human heart cDNA (YNakamura)"
/Cev_stage="adult"
/note="Organ: heart; normalized direction: from adult heart"
26 c 37 g 17 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                               GI:4810116
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Pred. No.
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Best Local
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7P05B09 Chromosome 7 Pla
7P05B09, mRNA sequence.
AA078527
AA078527.1 GI:1838015
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On Jun 5, 1998 this sequence version
Contact: Valle G.
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                                                                                              Genome Technology Branch
National Human Genome Research Institute/NIH
49 Convent Dr., MSC4431, Building 49, Room 2.
                                                                                                                                                                                        Touchman, J.W., Bouffard, G.G., Weintraub, L.A., Idol, J.R., Wang, L., Robbins, C.M., Nussbaum, J.C., Lovett, M. and Green, E.D. 2006 expressed-sequence tags derived from human chromosome 7-enriched cDNA libraries Genome Res. 7 (3), 281-292 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             o.1%;
l Similarity 100.0%;
37; Conservative
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Location/Qualifiers
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                Email: egreen@nhgri.nih.gov
Plate: 05 row: B column:
Seq primer: -21M13 (ABI)
                                                                                                                                            On Sep 12, 1996 this sequence version Contact: Eric D. Green
                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 96)
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                                                                Tel: 3014020201
Fax: 3014024735
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/db_xref="taxon:9606"
/clone="s4000013A06"
   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chiasce, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA252633 100 bp mRNA EST 12-MAR-1997 aq43g05.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone IMAGE:632504 5' similar to contains Alu repetitive element;contains element MER22 repetitive element; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 100)
                                                                                                                                                                                                                         Putative full length read
The vector to vector length is 101
Seg primer: -28ml3 revl ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On May 5, 1995 this sequence version replaced Contact: Wilson RK
                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Marra, M.
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//lab_host="E. coll strain DHS alpha"
//note="Organ: placenta; Vector: pAMP10; cDNA was generated from cytoplasmic RNA using a mixture of random DNA hexamers and oligo(dT). From this pool of cDNA, human chromosome 7-enriched cDNA was isolated by direct cDNA selection using chromosome 7 genomic DNA (cosmids). The resulting direct-selected cDNA was cloned into a plasmid vector using a non-directional uracil DNA glycosylase (UDG)-mediated cloning strategy."
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/db_xref="taxon:9606"
/clone="7P05B09"
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                                                        /db_xref="taxon:9606"
/clone="IMAGE:632504"
                                                                                                              /organism="Homo sapiens"
/db_xref="GDB:5182587"
                                                                                                                                                                                              Location/Qualifiers
  /clone_lib="Stratagene hNT neuron (#937233)"
/dev_stage="hNT neurons"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The WashU-Merck EST Project
Unpublished (1995)
On Apr 14, 1993 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 101)

1 (bases 1 to 101)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Parsons,J., Rohlfing,T., Soares,M., Tan,F., Rohlfing,T., Soares,M., Tan,F., Rohlfing,T., Soares,M., Tan,F., Rohlfing,T., Soares,M., Tan,F., Rohlfing,T., Rohlfing,T., Rohlfing,R., Rohlfing,R
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zal2a02.rl Soares fetal
IMAGE:292298 5' similar
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Fax: 314 286 1810
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37; Conservative
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Location/Qualifiers
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//note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dr.
Differentiated, post mitotic hNT neurons. Average insert
size: 1.5 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5'
GRAFTICGGCAGA 3' -3' adaptor sequence: 5'
CTCGAGTITTTTTTTTTTTTTTT 3'"
                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="GDB:3800071"
/db_xref="taxon:9606"
/clone="IMAGE:292298"
                                                                                                                                                                                                                                                                                                                                                                          /sex-"male"
                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Soares fetal liver spleen lNFLS"
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hes 37; Conservative
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1 (bases 1 to 74)

Touchman,J.W., Bouffard,G.G., Weintraub,L.A., Idol,J.R., Wang,L., Robbins,C.M., Nussbaum,J.C., Lovett,M. and Green,E.D.

2006 expressed-sequence tags derived from human chromosome 7-enriched cDNA libraries
Genome Res. 7 (3), 281-292 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: egreen@nhgri.nih.gov
Plate: 01 row: E column: 11
Seq primer: -21M13 (ABI).
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National Human Genome Research Institute/NIH
49 Convent Dr., MSC4431, Building 49, Room 2A08, Bethesda, MD 20892
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7T01E11 Chromosome 7 Th
7T01E11, mRNA sequence.
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                                                                                                                                                                                                               /Clone_lib="Chromosome 7 Thymus cDNA Library"
//sex="mixture of female and male"
/tissue_type="thymus"
/dev_stage="l week old (male), 11 year old (female)"
/dev_stage="l week old (male), 21 year old (female)"
/lab_host="E. coll strain DH5 alpha"
/note="Organ: thymus; Vector: pAMP10; cDNA was generated from cytoplasmic RNA using a mixture of random DNA hexamers and oligo(dT). From this pool of cDNA, human chromosome 7-enriched cDNA was isolated by direct cDNA selection using chromosome 7 genomic DNA (cosmids). The resulting direct-selected cDNA was cloned into a plasmid vector using a non-directional uracii DNA glycosylase (UDG)-mediated cloning strategy."

19 a 17 c 22 g 16 t
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/db_xref="taxon:9606"
/clone="7T01E11"
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

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Scoring table:

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821193 segs, -1518192014 residues

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Post-processing: Listing first

45 summaries

Minimum DB Maximum DB

seq length: 8 seq length: 105

Total number of hits satisfying

chosen parameters:

345848

Word size Searched:

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Search time 13412.9 Seconds (without alignments)
-6791.568 Million cell updates/sec
RESULT 1
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I3154 Sequence 43
I31518 Sequence 43
I31518 Sequence 34
I31153 Sequence 55
I31467 Sequence 2
A68621 Sequence 1
A68622 Sequence 1
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A68621 Sequence 31
I31400 Sequence 31
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K02284 Human poly
123536 Human chrom
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                  Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n method of using the same Patent: US 5582979-A 430 10-DEC-1996;
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Resnick,M.A., Larionov,V.L., Kouprina,N.Y. and Ferkins,E. TRANSFORMATION ASSOCIATED RECOMBINATION CLONING Patent: WO 9801573-A 15-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                         unidentified
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/db_xref="taxon:32644"
8 c 19 g
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25 c 0 g
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Sequence 1 from Patent WO9801573.
A68621
A68621.1 GI:4759648
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1 (bases 1 to 40)

Resnick, M.A., Larionov, V.L., Kouprina, N.
TRANSFORMATION-ASSOCIATED RECOMBINATION
Patent: WO 9801573-A 15-JAN-1998;
US HEALTH (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
36; Conserv
Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D. Alu RNA transcripts in human embryonal carcinoma copost-transcriptional selection of master sequences J. Mol. Biol. (1992) In press
                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 103)
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Resnick,M.A., Larionov,V.L., Kouprina,N.Y. and Perkins,E.L.
TRANSFORMATION ASSOCIATED RECOMBINATION CLONING
Patent: WO 9801573-A 15-JAN-1998;
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                                                                                            Homo sapiens male embryo carcinoma
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/db_xref="taxon:32644"
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artificial sequence.
1 (bases 1 to 35)
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inter-Alu specific primer DNA (pdj33) from patent WO9213101.
A25212
A25212.1 GI:904592
                                                                                                synthetic construct
synthetic construct
artificial sequence.
                                                                                                                                            inter-Alu specific A25212
                                                                                                                                                                                                                                                                                                                                               Patent:
                                                                                                                                                                                                                                                                                                                                   METHOD OF DETECTING DNA SEQUENCE VARIATION Patent: WO 9213101-A 3 06-AUG-1992; Location/Qualifiers
                                                             METHOD OF DETECTING DNA SEQUENCE VARIATION Patent: WO 9213101-A 3 06-AUG-1992;
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Similarity 100.0%;
35; Conservative (
                                                                                       ificial sequence. (bases 1 to 35)
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/dev_stage="embryo"
/sex="male"
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/db_xref="taxon:32630"
10 c 11 g 6 t
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/db_xref="taxon:9606"
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27 c 33 g 1
                /db_xref="taxon:32630"
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                                  organism="synthetic construct"
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Pred. No. 1.1e-05;
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DNA (pdj33) from patent WO9213101.
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19729 TGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGC 19763
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                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                              Andoreasu H.A., Yan F.;
"DETECTING METHOD FOR DNA ARRANGEMENT VARIATION";
Patent number JP 1995115999-A/3, 09-MAY-1995.
INGENII BV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JP 1995115999-A/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic DNA for Alu
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Artificial sequences.
JP 1995115999-A/3
09-MAY-1995
22-MAY-1992
7 1992130668
                                                                                                                                                                                                                                                                                                                          ANDOREASU HERARUDOUSU AITSUTERURINDEN, YA C12Q1/68,C12N15/00,G01N27/447,G01N27/447; strandedness: Single;
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ilarity 100.0%;
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llarity 100.0%; F
Conservative 0;
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A;
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                                                                                                                                                /organism="unidentified"
                                                                                                                                                              /db_xref="taxon:32644"
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                                                                                                                      10 C; 11 G;
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                                                                                                                                                                                                                               /note="Alu specific primer"
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1. .35
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Last updated, Version
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Pred. No.
                                                     Score 35; DB 24;
Pred. No. 1.1e-0
0; Mismatches
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                                                                    1.1e-05;
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standard; DNA; UNC;

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E09140;

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DEFINITION
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HUMUT8164A/c
LOCUS H
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 TITLE
                                             AUTHORS
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                                                                                                                                                                                                                                                                                                                                     Sequence 35 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Andoreasu H.A., Yan F.; "DETECTING METHOD FOR DNA ARRANGEMENT VARIATION"; Patent number JP 1995115999-A/3, 09-MAY-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unidentified unclassified
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08-OCT-1997 (Rel. 52, Last upd
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Artificial sequences.
Jp 1995115999-A/3
09-MAY-1995
22-MAY-1992 JP 1992130668
22-MAY-1992 JP 1992130668
ANDOREASU HERARUDOUSU AITSUTERURINDEN, YACTIOL/68,C12N15/00,G01N27/447,G01N27/447;
strandedness: Single;
                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  topology: Linear;
                                                                                        L30244.1 GI:605447
STS; PCR primer; STS sequence; microsatellite DNA; microsatellite
marker; sequence tagged site; tetranucleotide repeat.
Homo sapiens DNA.
                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 91)

1 (bases 1 to 91)

Gerken, S.C., Matsunami, N., Plaetke, R., Albertsen, H., Ballard, L., Melis, R., Lawrence, E., Moore, M., Holik, P.R., Carlson, M., Zhao, X., Robertson, M., Bradley, P., Elsner, T., Tingey, A., Lalouel, J.-M. and
                                                                                                                                                  Human STS UT8164,
L30244
Genetic and physical mapping of simple sequence
                                                                                                                                                                          HUMUT8164A
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64, 5'
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Pred. No.
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rch completed:
time: 223289 s
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35; Conserv
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Primer A: AGAGGTTGCAGTGAACCAA
Primer B: TTTTCCCCCTCTACTCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted by: Utah Center for Human Genome Utah, Dept. of Human Genetics 2160 Eccles Institute of Human Genetics Salt Lake City, UT 84112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence tagged sites from the human genome Unpublished (1994)
                                                                                                                                                                                                                                                                                           Alleles:
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Initial Denaturation: 94C 300sec
Cycles Denaturation Annealing
Cycles Denaturation 72C 20
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10 sec. 56 C 10 sec. 70 sec. 52 C 10 sec. 72 C 20 sec. Mg++: 1.50 r
el: Acrylamide 7%, Formamide 32%, Urea 34%
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: March
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                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
10. .28
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20 c 23 g
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             31,
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Pred. No.
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Microsatellite seq Microsatellite seq Microsatellite seq Microsatellite seq Microsatellite seq Repeat sequence fr Repeat sequence fr

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Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic search, using sw model
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30001
1 AGTGAATATTTATAGAGTCC......GCAG
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Copyright (c) 1993 - 2000 Com
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Inter-Alu specific Inter-Alu specific Sequence of a micr Repeat sequence fr Microsatellite seq Repeat sequence fr Repeat sequence fr Sequence of a micr Sequence of a microsatellite seq Microsatellite seq Microsatellite seq Poly GT enhancer e Sequence of a microsatellite seq Poly GT enhancer e Sequence of a microsatellite seq Poly GT enhancer e Sequence of a microsatellite seq Poly GT enhancer e Sequence of a microsatellite seq Poly GT enhancer e Sequence of a microsatellite seq Poly GT enhancer e Sequence of a microsatellite seq Poly GT enhancer e Sequence of a microsatellite seq Poly GT enhancer e Sequence of a microsatellite seq Poly GT enhancer e Sequence of a microsatellite seq Poly GT enhancer e Sequence of a microsatellite seq Poly GT enhancer e Sequence of a microsatellite seq Poly GT enhancer e Sequence e Sequence of a microsatellite seq Poly GT enhancer e Sequence e Seq
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Repeat sequence fr
Repeat sequence fr
(dC-dA)n.(dG-dT)n
Repeat sequence fr
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Repeat sequence fr
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V39744/c
TD V39744 standard; cDNA; 88
                                                     PT Sequencing nucleic acids by mass spectrometric analysis - for detecting nucleic acids, telomerase activity, oncogene mutations, or processes of the sequences, for diagnosis of disease example li; page 318; 478pp; English.

CC Aprocess has been developed for determining the sequence of a target complete acid. The process comprises: (1) generating at least two craments (F) from the target nucleic acid; and (ii) analysing F by compared primers for use in the mass spectrometric diseases. The process is used to detect genetic diseases comprises: (1) generating at least two specifically claimed primers for use in the mass spectrometric analysis of the above process. The process is used to detect genetic diseases comprises; (1) generation dystrophy, Alzhelmer's (2) generations; infections and cancers; also for establishing compared specifically. Particular applications are diagnosis of converblastoma, detecting telomerase, determining family relationships and HIAA comparibility, and in genetic fingerprinting. Compared with known methods using MS, this process requires fewer specific reagents cand is better suited to automation. Extended primers are shorter; primer annealing is more efficient and the process allows detection of conjugation of the process sample from the present invention.

Sequence 88 BP; 56 A; 5 C; 7 G; 20 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-MAY-1998.
06-NOV-1997; US-947801.
08-OCT-1997; US-947801.
06-NOV-1996; US-744481.
06-NOV-1996; US-746390.
06-NOV-1996; US-746055.
23-JAN-1997; US-786398.
23-JAN-1997; US-7873392.
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Van Den Boom D, Xiang G;
WPI; 98-286975/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Microsatellité analysis antisense strand SEQ ID NO:262.
Mass spectrometry; diagnosis; detection; biological sample; infection; genetic disease; chromosomal abnormality; identification; heredity; pathogenic organism; telomerase activity; oncogene mutation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SEQU-) SEQUENOM INC.
Braun A, Damhoffer-Demar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
WO9820166-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer-specific sequence; primer; ss.
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Q33773
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Q33921
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T65744
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Minimum DB Maximum DB

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length: 8 length: 105

Post-processing: Listing first

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Query Match

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Microsatellite seq Repeat sequence Sequence of a micr

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Query Match
Best Local Similarity
Matches 63; Conserv

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Score 63; DB Pred. No. 5.8 0; Mismatches

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Gaps

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Word size

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Scoring table:

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Title: Perfect score:

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                                                                                                                                                                                                                                                                                                                                    PT Detection of polymorphic genetic markers of the form
pr (dC-dA)n(dG-dT)n - using novel nucleic acid mols as primers
ps Disclosure; Column 11-12; 186pp; English.

CC The invention relates to the isolation of polymorphic repeat sequences
cC thaving the sequence (dC-dA)n.(dG-dT)n which can be used as genetic
cc markers. Primers based on these sequences can be used to detect these
cC repeats, especially for use in e.g paternity or maternity testing,
cc human genetic analysis such as linkage analysis of genetic disease,
cc containing the repeat sequences were isolated by hybridisation of
cc containing the repeat sequences were isolated by hybridisation of
cc cromosome-specific phage libraries with a synthetic poly(dC-dA), (dG-dT)
crobe. Over 100 repeat blocks were isolated. The inserts from the clones
cc were amplified by primers T65798-T66047. Those clones where the repeat
cc sequence has been determined are shown in T65704-797. This repeat
cc sequence is from the marker clone Mdf67 which contains the repeat
cc sequence having the formula: (TC)12(AC)18.
So Sequence 60 BP; 18 A; 30 C; 0 G; 12 T;
                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 54
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21-APR-1989;
21-APR-1989;
05-SEP-1991;
04-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-APR-1989;
21-APR-1989;
05-SEP-1991;
04-APR-1994;
                                                                                             Repeat sequence from polymorphic marker clone Mfd39.
Polymorphism; repeat sequence; genetic marker; primer; amplification;
PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
US5582979-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat sequence from polymorphic marker clone Mfd67.
Polymorphism; repeat sequence; genetic marker; primer; amplificati
PCR; polymerase chain reaction; paternity; maternity; human; pedig
linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                            US5582979-A.
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                                                                                  hybridisation; chromosome;
                                                                                                                                                                     T65740 standard; DNA;
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US-341562.
US-754351.
US-222177.
341562.
US-341562.
US-754351.
US-222177.
                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                        0.2%;
                                                                                                                                                                      91 BP
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                                                                                     ds
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                                                                                                                                                                                                                                                                                         Score 54;
Pred. No.
                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                   Length 60
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RESULT
T66081
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PT Detection of polymorphic genetic markers of the form [dC-dA)n(dC-dT)n - using novel nucleic acid mols. as primers PT (dC-dA)n(dC-dT)n - using novel nucleic acid mols. as primers PS Example 8; Column 57-58; 186pp; English.

CC The invention relates to the isolation of polymorphic repeat sequences CC having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic CC markers. Primers based on these sequences can be used to detect these CC markers. Primers based on these sequences can be used to detect these CC markers. Primers based on these sequences can be used to detect these CC commercial animal or plant breeding or pedigree analysis of genetic disease, CC commercial animal or plant breeding or pedigree analysis.

CC 1) perfect repeats which are alternating tandem CA repeats with no CC interruptions and without adjacent repeats of another sequence; CC 2) imperfect repeats which are defined as 2 or more runs of uninterrupted CC 3) compound perfect repeats which are uninterrupted runs of CA separated by no more than 3 consecutive non-repeat bases; CC 3) compound perfect repeats which are uninterrupted runs of CA separated by no more than 3 consecutive non-repeat bases from a run of at least CC (dC-dA)n (dG-dT)n, or from at least 10 uninterrupted mononucleotides; and CC injureriect compound repeats which are defined as for the perfect compound repeats except that the runs of CA are interrupted.

CC This sequence is an example of a compound imperfect repeat sequence of structure: T(CT)12GTT(TC)11T(CA)14A(AC)6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pr Detection of polymorphic genetic markers of the form pr (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers Disclosure; Column 9-10; 186pp; English.

CC The invention relates to the isolation of polymorphic repeat sequences CC having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic CC markers. Primers based on these sequences can be used to detect these CC repeats, especially for use in e.g paternity or maternity testing, CC human genetic analysis such as linkage analysis of genetic disease, CC commercial animal or plant breeding or pedigree analysis. Clones CC containing the repeat sequences were isolated by hybridisation of CC chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) CC grobe. Over 100 repeat blocks were isolated. The inserts from the clones CC were amplified by primers T65798-T66047. Those clones where the repeat CC sequence has been determined are shown in T65704-797. This repeat CC sequence is from the marker clone Mdf39 which contains the repeat CC sequence having the formula: (TC)12.5GTT(TC)11.5(CA)14A(CA)5.5.
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Best Local S
Matches 50
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10-DEC 1996.
21-APR-1989; 341562.
21-APR-1989; US-341562.
21-APR-1989; US-754351.
05-SEP-1991; US-754351.
04-APR-1994; US-722177.
(MARS-) MARSHFIELD CLINIC.
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Weber J
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Polymorphism; repeat sequence; genetic marker; primer; amplification;
PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
Linkage analysis; genetic disease; animal; plant; breeding; locus;
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llarity 100.0%;
Conservative
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Pred. No.
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hes 0;
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                                                                                                                                                                                                                                                       PT Detection of polymorphic genetic markers of the form
PT (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers
PS Disclosure; Column 13-14; 186pp; English.
CC The invention relates to the isolation of polymorphic repeat sequences
CC having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic
CC markers. Primers based on these sequences can be used to detect these
CC comman genetic analysis such as linkage analysis of genetic disease,
CC commercial animal or plant breeding or pedigree analysis. Clones
CC containing the repeat sequences were isolated by hybridisation of
CC chromosome-specific phage libraries with a synthetic poly(dC-dA).(dG-dT)
CC grobe. Over 100 repeat blocks were isolated. The inserts from the clones
CC were amplified by primers T65798-T66047. Those clones where the repeat
CC sequence has been determined are shown in T65704-797. This repeat
CC sequence is from the marker clone Mdfil0 which contains the repeat
CC sequence 46 BP; 12 A; 0 C; 0 G; 34 T;
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Best Local S
Matches 50
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Best Local
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10-DEC-1996.
21-APR-1989; 341562.
21-APR-1989; US-341562.
21-APR-1991; US-754351.
04-APR-1994; US-222177.
                                                                                                                                                             Homo sapiens.
US5582979-A.
10-DEC-1996.
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                                         Repeat sequence from polymorphic marker clone Mfd5.
Polymorphism; repeat sequence; genetic marker; primer; amplification;
PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                T65707 standard;
T65707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Repeat sequence from polymorphic marker clone Mfd110;
Polymorphism; repeat sequence; genetic marker; primer; amplification;
PCR; polymerase chain reaction; paternity; maternity; human; pedigree;
linkage analysis; genetic disease; animal; plant; breeding; locus;
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                                                                                      17-JUN-1997 (first entry)
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                                  hybridisation;
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                                                                                                                                                                                                         46;
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                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                         Conservative
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                                                                                                           DNA;
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                                                                                                           56 BP
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Pred.
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0.0015;
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pr detection of polymorphic genetic markers of the form
pr (dd-dA)n(dG-dT)n - using novel nucleic acid mols. as primers
Claim 1; Column 13-14; 186pp; English.

CC The invention relates to the isolation of polymorphic repeat sequences
CC The invention relates to the isolation of polymorphic repeat sequences
CC markers. Primers based on these sequences can be used as genetic
CC markers. Primers based on these sequences can be used to detect these
CC repeats, especially for use in e.g paternity or maternity testing,
CC human genetic analysis such as linkage analysis of genetic disease,
CC containing the repeat sequences were isolated by hybridisation of
CC containing the repeat sequences were isolated by hybridisation of
CC chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT)
CC corobe. Over 100 repeat blocks were isolated. The inserts from the clones
CC were amplified by primers T65798-T66047. Those clones where the repeat
CC sequence has been determined are shown in T65704-797. This repeat
CC sequence is from the marker clone Mdf120 which contains the repeat
CC sequence 50 BP; 20 A; 25 C; 0 G; 5 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PT Detection of polymorphic genetic markers of the form
PT (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers
PT (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers
PT (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers
PT (dC-dA)n (dG-dT)n - using novel nucleic acid mols. as primers
PT (dC-dA)n - (dG-dT)n - using novel nucleic acid mols. as primers
PT (dC-dA)n - (dG-dT)n - using novel nucleic acid mols. as primers
PT (dC-dA)n - (dG-dT)n - using nucleic acid mols.
PT (dC-dA)n - (dG-dT)n - using nucleic acid mols.
PT (dC-dA)n - (dG-dT)n - using nucleic acid mols.
PT (dC-dA)n - (dG-dT)n - using nucleic acid mols.
PT (dC-dA)n - using nucleic acid m
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Best Local S
Matches 42
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21-APR-1989; US-341562.
05-SEP-1991; US-754351.
04-APR-1994; US-222177.
(MARS-) MARSHFIELD CLINIC.
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21-APR-1989; U
05-SEP-1991; U
04-APR-1994; U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Repeat sequence from polymorphic marker clone Mfd120. Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 97-042299/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hybridisation;
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; US-341562.
; US-754351.
; US-222177.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      chromosome;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLINIC
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RESULT
Q33779
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                                                                                                                                                                                                                                                                                                                                                                                                  PT Polymorphic bovine DNA markers - used in genetic identification,
PT gene mapping, and selective breeding
PS Table 7; Page 170; 517pp; English.

CC The sequence is that of a bovine microsatellite sequence obtd. by
CC screening a library of bovine MboI DNA fragments of between
CC 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.
CC one out of 50 clones cross-hybridised. Assuming independent
CC distribution of microsatellites and MboI sites, the frequency of
CC (T6)n > microsatellites in the bovine genome is estimated at >100,
CC 000. The sequence information for ca. 230 such bovine microsatellites
CC is summarised in the specification and indexed herein (see below).
CC The sequences upstream and downstream of the microsatellite sequence
CC were used to generate the required PCR primers for in vitro
CC amplification of the corresp. microsatellite sequence
CC amplification of the corresp. microsatellite (using the program
CC optified of the corresp. microsatellite in the program
CC or parentage testing, and in the genetic mapping of economic trait
CC loci, or genes involved the determinism of economic trait
CC craits esp. in cattle, to allow selective breeding.
Sequence 56 BP; 19 A; 0 C; 28 G; 9 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 41
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 41; Conser
                                                                                                                                                                                                                                                                    Microsatellite sequence from clone TGLA PCR; selection; primers; OPTIPRIM; bree genetic mapping; traits; amplification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GENM-) GENMARK.
Georges M, Massey JM;
WPI; 92-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-FEB-1993 (first entry)
Microsatellite sequence from clone AGLA296.
PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
(GENM-) GENMARK.
Georges M, Massey JM;
WPI; 92-284684/34.
                                        W09213102-A.
06-AUG-1992.
15-JAN-1992; U00340.
15-JAN-1991; US-642342.
                                                                                                                                                                                             Q33779 standard; DNA; 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q33603 standard; DNA; 56
                                                                                                      Bos taurus
                                                                                                                                                                                Q33779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-AUG-1992.
                                                                                                                                                                 02-FEB-1993
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15-JAN-1991; US-642:
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ilarity 100.0%;
Conservative (
                                                                                                                                                               (first entry)
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                                                                                                                  breeding;
tion; ss.
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0.027;
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0.028;
                                                                                                                               cattle; parentage,
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CC The sequence is that of a bovine microsatellite sequence obtd. by CC screening a library of bovine MboI DNA fragments of between CC 250 and 500 bp with an (AC)15 and a (TC)15 olligonucleotide probe. CC One out of 50 clones cross-hybridised. Assuming independent CC distribution of microsatellites and MboI sites, the frequency of CC (T6)n > microsatellites in the bovine genome is estimated at >100, CC is summarised in the specification and indexed herein (see below). CC The sequence upstream and downstream of the microsatellite sequence were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program CC oppirprimy). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait CC craits esp. in cattle, to allow selective breeding.

See also Q33501-34437.

Se Sequence 62 BP; 42 A; 0 C; 31 G; 9 T;
                                                                                                                                   gene mapping, and selective breeding
Table 7; Page 167; 517pp; English.
Cathe sequence is that of a bovine microsatellite sequence obtd. by
Cathe sequence is that of a bovine microsatellite sequence obtd. by
Cathe sequence is that of a bovine microsatellite sequence obtd. by
Cathe sequence is that of a bovine microsatellites of between
Cathe sequence information for ca. 230 such bovine microsatellites
Cathe sequence upstream and downstream of the microsatellites
Cathe sequences upstream and downstream of the microsatellite sequence
Camplification of the corresp. microsatellite (using the program
Camplification of the microsatellites may be used to identify individuals,
Cathe sequence information in the sequence used to represent the required PCR primers for in vitro
Camplification of the corresp. microsatellite (using the program
Cathe sequence information in the sequence were used to generate the required PCR primers for in vitro
Cathe sequence information in the sequence were used to generate the required PCR primers for in vitro
Cathe sequence information in the sequence were used to generate the required PCR primers for in vitro
Cathe sequence information in the sequence were used to generate the required PCR primers for in vitro
Cathe sequence information in the sequence were used to generate the required PCR primers for in vitro
Cathe sequence information in the sequence in the program i
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Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09213102-A.
06-AUG-1992.
15-JAN-1992; U00340.
15-JAN-1991; US-642342.
(GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Microsatellite sequence from clone AGLA29. PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss. Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q33594 standard; DNA; 63 BP
Q33594;
traits esp. in cattle, to allow see also Q33501-34437. Sequence 63 BP; 22 A; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Georges M, Massey JM;
WPI; 92-284684/34.
                                                                                for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polymorphic bovine DNA markers - used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                        selective breeding.
     32
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0.026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genetic identification,
  <u>ი</u>
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Query Match Best Local S Matches 41

Similarity

0.1%; llarity 100.0%; Conservative (

%; Score 41; DB
%; Pred. No. 0.0
0; Mismatches

DB 1; 0.026;

Length 63

0

Gaps

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28932

28972

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pri gene mapping, and selective breeding

Pri gene mapping, and selective breeding

RS Table 7; Page 176; 517pp; English.

CC The sequence is that of a bovine microsatellite sequence obtd. by

CC screening a library of bovine MbcI DNA fragments of between

CC 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.

CC One out of 50 clones cross hybridised. Assuming independent

CC distribution of microsatellites and MbcI sites, the frequency of

CC (T6)n > p microsatellites in the bovine genome is estimated at >100,

CC 000. The sequence information for ca. 230 such bovine microsatellites

CC is summarised in the specification and indexed herein (see below).

CC The sequences upstream and downstream of the microsatellite sequence

CC were used to generate the required PCR primers for in vitro

CC amplification of the corresp. microsatellite using the program

CC OPTIPRIM). The microsatellites may be used to identify individuals,

CC for parentage testing, and in the genetic mapping of economic trait

CC loci, or genes involved the determinism of economically important

CC see also 033501-34437.

Sequence 40 BP; 11 A; 0 C; 20 G; 9 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 0.1%;
Best Local Similarity 100.0%;
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          Variability (first entry)
Microsatellite sequence from clone AGLA8.
PCR: selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
Bos taurus.
Kouprina NY, Larionov VL, Perkins EL, Resnick MA; WPI; 98-110234/10.

Preparation of yeast artificial chromosomes - by in vivo recombination using vector comprising yeast centromere, myeast telomere and nucleic acid for recombination Example 1; Page 45; 117pp; English.
                                                                            15-JAN-1998.
15-JAN-1998.
09-JUL-1996; W0-U11478.
09-JUL-1996; WO-U11478.
(USSH) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENM-) GENMARK.
Georges M, Massey JM;
WPI; 92-284684/34.
                                                                                                                                                                                                                          circular yeast
                                                                                                                                                                                                                                        Alu PCR primer 2. PCR; primer; amplification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-AUG-1992.
15-JAN-1992; U00340.
15-JAN-1991; US-642342.
                                                                                                                                                                         Saccharomyces sp. WO9801573-A1.
                                                                                                                                                                                                                                                                                            V19045;
                                                                                                                                                                                                                                                                                                         V19045 standard; DNA; 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polymorphic bovine DNA markers - used in genetic identification
                                                                                                                                                                                                                                                                         28-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                              6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                                                                                                        artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA;
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                                                                                                                                                                                                                      n; Alu repeat sequence; vector;
chromosome; YAC; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
0.053;
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                                         marker,
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B S E

V19044 standard; DNA; 40 V19044; 28-JUL-1998 (first entry

(first entry)

RESULT 14 V19044

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Matches Query Match Best Local

Local

. Similarity 38; Conser

Conservative

0

Mismatches

Indels

0

Gaps

0

0 B B 1; 0

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RESULT 1
Q33534/c
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                                                                                 ននិនិនិនិនិនិនិនិ
                                                                     PT Polymorphic bowine DNA markers - used in genetic identification, program appling, and selective breeding fable 7: Page 141; 517pp; English.

CC The sequence is that of a bowine microsatellite sequence obtd. by cc screening a library of bowine MboI DNA fragments of between CC 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. CC One out of 50 clones cross-hybridised. Assuming independent CC (15)n >9 microsatellites and MboI sites, the frequency of CC (75)n >9 microsatellites in the bowine genome is estimated at >100, CC (00). The sequence information for ca. 230 such bowine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence camplification of the corresp. microsatellite (using the program CC were used to generate the required PCR primers for in vitro amplification of the corresp. microsatellite (using the program CC oppirRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait CC traits esp. in cattle, to allow selective breeding.

See also Q33501-34437.

So Sequence 64 BP; 19 A; 1 C; 30 G; 14 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This is the nucleotide sequence for the PCR primer used in the amplification of the Alu repeat sequence, which is used to demonstrate the processes described in the invention. It involves the creation and use of circular yeast artificial chromosome (YAC) to selectively clone specific nucleic acids from a background of mixed nucleic acids by introducing the vector(s) into E. coli cells. They can be used to rapidly isolate human DNA where only a part of t sequence of DNA is known. Using the methods large fragments of DNA be easily cloned and analysed.

Sequence 40 BP; 9 A; 8 C; 19 G; 4 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GENM-) GENMARK.
Georges M, Massey JM;
WPI; 92-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Microsatellite sequence from clone AGLA226.
PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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15-JAN-1991;
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0.1%;
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Score 38; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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Pred. No.
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0.053;
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                  Length 64;
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Saccharomyces sp. W09801573-A1. 15-JAN-1998.

Synthetic

Alu PCR primer 1.
PCR; primer; amplification; Alu repeat sequence; circular yeast artificial chromosome; YAC; ss.

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RESULT 15
V19044/c
ID V419044; standard; DNA; 40 BI
AC V19044;
DT 28-JUL-1998 (first entry)
DE Alu PCR primer 1.
KW PCR; primer; amplification;
KW circular yeast artificial (
OS Synthetic.
OS Saccharomyces sp.
PN W09801573-A1.
PD 15-JAN-1998; U11478.
PR 09-JUL-1996; WO-U11478.
PR 09-JUL-1996; WO-U11478.
PR (USSH) US DEFF HEALTH 6 HI
PI Kouprina NY, Larionov VL, J
DR WPI; 98-110234/10.
PT Preparation of yeast artification using vector yeast telomere and nucleic PS Example 1; Page 45; 117pp; CC This is the nucleotide sequence of DNA is known.
CC the creation and use of cit to selectively clone specific comixed nucleic acids by intice to sequence of DNA is known.
CC sequence 40 BP; 7 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
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PT Preparation of yeast artificial chromosomes - by in vivo
PT recombination using vector comprising yeast centromere, marker,
PT yeast telomere and nucleic acid for recombination
PS Example 1; Page 45; 117pp; English.

CC This is the nucleotide sequence for the PCR primer used in the
CC amplification of the Alu repeat sequence, which is used to
Cd demonstrate the processes described in the invention. It involves
CC the creation and use of circular yeast artificial chromosome (YAC)
CC to selectively clone specific nucleic acids from a background of
CC mixed nucleic acids by introducing the vector(s) into E. coli cells.
CC They can be used to rapidly isolate human DNA where only a part of the
CC sequence of DNA is known. Using the methods large fragments of DNA can
Commence And C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 36; Conserv
  Query Match 0.1%; Sometime 0.0%; 18 Sest Local Similarity 100.0%; 19 Matches 36; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preparation of yeast artificial chromosomes - by in vivo recombination using vector comprising yeast centromere, marker, yeast telomere and nucleic acid for recombination Example 1; Page 45; 117pp; English.

This is the nucleotide sequence for the PCR primer used in the amplification of the Alu repeat sequence, which is used to demonstrate the processes described in the invention. It involves the creation and use of circular yeast artificial chromosome (YAC) to selectively clone specific nucleic acids from a background of mixed nucleic acids by introducing the vector(s) into E. coli cells. They can be used to rapidly isolate human DNA where only a part of the sequence of DNA is known. Using the methods large fragments of DNA can be passive cloned and analysed.
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PCR; primer; amplification; Alu repeat sequence;
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Patent No.
  Query Match
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APPLICANT: Weber,
                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                            IMMEDIATE SOURCE:
CLONE: mfd67rs
                                                                                                                                                                  MOLECULE TYPE:
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                                                                                                                                                                                                                                            TYPE: nucleic acid
                                                                                                                                                                                                  TOPOLOGY:
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Sequence 101, App	Sequence 364, App	Sequence 203, App	Sequence 157, App	Sequence 249, App	Sequence 241, App	Sequence 195, App	Sequence 388, App	Sequence 370, App	Sequence 229, App	Sequence 53, Appl	Sequence 232, App	Sequence 183, App	Sequence 74, Appl	Sequence 403, App	Sequence 400, App	Sequence 119, App	Sequence 137, App	Sequence 397, App

ALIGNMENTS

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US-08-222-177A-244
US-08-222-177A-244
US-08-222-177A-244
PREDICANT: Weber; James L.
APPLICANT: Weber; James L.
APPLICANT: Weber; James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 460
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dewlitt Ross & Stevens, S.C.
STREET: 8000 Excelsior Drive, Suite 401
CITY: Maddson
STATE: Wisconsin
COUNTRY: USA
ZIP: 53717-191 GAR
ZIP: 53717-191 GAR
COMPUTER READABLE FORM:
MEDIUM TYPE: LDAPPY disk
COMPUTER READABLE FORM:
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COMPUTER READABLE FORM:
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APPLICATION NUMBER: US/08/222.177A
FILING DATE: 21-APR-1989
ATTORNET/AGENT INFORMATION:
REGISTRATION WUMBER: 30,492
REFERENCE/DOCKET NUMBER: 30,492
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                                        Sequence 430, Application US/08222177A Patent No. 5582979
GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1999
ATTORNEY_AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 09.492
REFERENCE/DOCKET NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: US
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MEDIUM TYPE: Floppy disk
APPLICANT: Weber, James L. TITLE OF INVENTION: LENGTH TITLE OF INVENTION: (dC-dA
                                                                                                                                                                                                                                                                                                                                TOPOLOGY: 1. MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
CLONE: mfd39rs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ITLE OF INVENTION: LENGTH POLYMORPHISMS IN ITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                   30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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                                                                                                                                                  53717-1914
                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                         91 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/08222177A
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                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                double
                                                                                                                                                                                                                         0.2%;
LENGTH POLYMORPHISMS IN (dC-dA)n \cdot (dG-dT)n SEQUENCES AND METHODS OF USING SAME
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mismatches 0;
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US-08-222-177A-430
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Best Local S
Matches 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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LENGTH: 92 base pairs
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
COPTRAINES: Patagett Patagett
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                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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                                 FILING DATE:
                                                                                                                                                                    COUNTRY: USA
ZIP: 53717-1914
                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                        CITY: Madison
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IOR APPLICATION: 435
                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                          ADDRESSEE:
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nucleic acid
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8000 Excelsior Drive, Suite 401
                                                                                                                                                                                                                                      E: DeWitt Ross & Stevens, S.C.
8000 Excelsior Drive, Suite 401
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                                                                                                                                                                                                                                                                                                                                              James L
                                                                                                                                                                                                                                                                                        LENGTH POLYMORPHISMS IN (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING 460
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APPLICATION NUMBER: US 07/341,562 FILING DATE: 21-APR-1989

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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 0986
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                       ZIP: 53717-1914

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                             NAME: Sara, Charles S. REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                             CLASSIFICATION: 435
PAPPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
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STATE: Wisconsin
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 STRANDEDNESS:
                                ENGTH:
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                              56 base pairs
                                                                                                (608) 831-2106
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100.0%; Pred. No. 3.9e-06;
n. Mismatches 0;
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RESULT

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Best Local Similarity
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;; IMMEDIATE SOURCE:
; CLONE: mfd5rs
US-08-222-177A-65
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                                                         Query Match 0.1%; S
Best Local Similarity 100.0%; Matches 41; Conservative 0;
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                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UDATA:
US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: SATA, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION: APPLICANT: Weber,
                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA IMMEDIATE SOURCE: CLONE: mfd120rs
                           COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,177A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 50 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH
TITLE OF INVENTION: (dC-dA
                                                                                                                                                                                                        STRANDEDNESS:
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CITY: Madison
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8000 Excelsior Drive, Suite 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                               (608) 831-2106
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                                                         Score 41; DB; Pred. No. 0.
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Pred. No.
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                                                                                      Length 50
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RESULT 8
US-08-222-177A-175
; Sequence 175, Application US/08222177A
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Patent No. 5582979

GENERAL INFORMATION:
APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 460
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                 atent No. 5582979
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 091
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
TELEPAX: (608) 831-2106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                         APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dc-da)n.(dg-dT)n SEQUEN
NUMBER OF SEQUENCES: 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMEDIATE SOURCE:
CLONE: mfd97rs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/222,177A FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
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                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
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                                                                                                        ADDRESSEE:
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                    53717-1914
                                                                       Madison
READABLE FORM
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                                                     Wisconsin
                                                                                8000 Excelsior Drive, Suite 401
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8000 Excelsior Drive, Suite 401
                                    USA
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                                                                                                        DeWitt Ross & Stevens, S.C
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                                                                                                                                                          (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
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100.0%; Pred. No.
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Query Match
Best Local Similarity
Matches 33; Conserva
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; CLONE: mfd42rs
US-08-222-177A-175
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APPLICATION NUMBER: US 07/341
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                               FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Weber,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                               CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: DeWitt Koss & Sterene, Street: 8000 Excelsion Drive, Suite 401
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5. 5582979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH POLYMORPHISMS IN (dC-dA)n. (dG-dT)n SEQUENCES AND METHODS OF USING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US 07/341,562
                                                                                                                                                                                        US/08/222,177A
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                   09865.601
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0.054;
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US-08-222-177A-317
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; MOLECULE TYPE:
US-08-222-177A-71
                                                                                   US-08-222-177A-317
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Query Match 0.1%; Score 33; DB Best Local Similarity 100.0%; Pred. No. 0. Matches 33; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 46 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                  TOPOLOGY: linea MOLECULE TYPE: DN IMMEDIATE SOURCE: CLONE: mfd99rs
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA
APPLICATION NUMBER: US/08/222,177A
                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 51 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: DeWitt Ross & Stevens, S.C.
STREET: 8000 Excelsion Drive, Suite 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: LENGTH POLYMORPHISMS IN TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENUMBER OF SEQUENCES: 460
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nes 33; Conserva
                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                 TELEFAX: (608) 831-2106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Wisconsin
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(608) 831-2106
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                 DB 1;
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                                  Length 51;
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Sequence 45, Application US/08267803B
Patent No. 5834183
GENERAL INFORMATION:
APPLICANT: OTI, Harry T.
APPLICANT: Ranum, Laura P.M.
APPLICANT: Cohung, Ming-yi
APPLICANT: Zoghbi, Huda Y.
TITLE OF INVENTION: Gene Sequence for the sequence of the sequence o
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US-08-469-802B-27
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APPLICANT: Ranum, Laura P.W.

APPLICANT: Chung, Ming-yi

APPLICANT: Zoghbi, Huda Y.

TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia

Patent No. 5741645
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 612-305-1225 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28954 CACACACACACACACACACACACACACACAT 28986
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,802B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 612-305-1217
TELEFAX: 612-305-1225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Mueting, Ann M.
REGISTRATION NUMBER: 33,
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NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mueting, Raasch, Gebhardt & Schwappach, P.A.
STREET: 119 No. 5741645th Fourth Street, Suite 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: 1: MOLECULE TYPE:
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MEDIUM TYPE: Floppy
TITLE OF INVENTION:
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LENGTH: 54 base pairs
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STATE: MN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27, Application US/08469802B
5, 5741645
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Type 1 and Method for Diagnosis
                                                                                   Gene Sequence for Spinocerebellar Ataxia
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NUMBER OF SEQUENCES: 85
CORRESSEE: Mueting, Raasch, Gebhardt & Schwappach, P.A.
STREET: P.O. Box 581415

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5506118-3
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5506118-3/c
; PATENT NO. 5506118
; PATENT NO. 5506118
; PAPPLICANT: BERG, DAVID T.; GRINNELL, BRIAN W.
; TITLE OF INVENTION: METHOD OF USING EUKARYOTIC EXPRESSION
; VECTORS COMPRISING A POLY GT ELEMENT IN THE PRESENCE OF
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                                                                                                                                                                                                FILING DATE: 07-OCT-1988 SEQ ID NO:3:
                                                                                                                                                                                                                                                                                                                                                                   TRANS-ACTING GENE PRODUCTS
NUMBER OF SEQUENCES: 1:
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Best Local S
Matches 33
                                                                                     Query Match
Best Local Similarity
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                                28953 TCACACACACACACACACACACACACACACA 28985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: MCCOTMACK, MYTA H.
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 110.00030120
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEPHONE: 612-305-1228
TELEPAX: 612-305-1228
                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/110,475
FILING DATE: 23-AUG-1993
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 54 base pairs
                                                                                                                                                                                                                                       FILING DATE: 15-JUL-1992
APPLICATION NUMBER: 255,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/267,803B FILING DATE: 28-JUN-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Minneapolis
                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 914,651
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TCACACACACACACACACACACACACACACA 21
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100.0%; Pred. No. 0.051;
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100.0%; Pred. No.
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; TOPOLOGY: linea;
; MOLECULE TYPE: DN.
; IMMEDIATE SOURCE:
; CLONE: mfd3rs
US-08-222-177A-59
                                                                                                               Sequence 218, Application US/082; Patent No. 5582979; Patent No. 5582979; GENERAL INFORMATION: APPLICANT: Weber, James L. TITLE OF INVENTION: (dC-dA)n NUMBER OF SEQUENCES: 460
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US-08-222-177A-59
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Best Local :
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION: APPLICANT: Weber,
                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,177A
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                   CORRESPONDENCE ADDRESS
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                                                                   STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (608) 831-2106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                               STATE: Wisconsin
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                                                                                     ADDRESSEE:
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               COUNTRY:
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32; Conserv
RY: USA
53717-1914
                                                     Madison
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                                                              E: DeWitt Ross
8000 Excelsion
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                                                                                                                                                                                                                        Application US/08222177A
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                                                                                                                                   LENGTH POLYMORPHISMS IN (dC-dA)n (dG-dT)n SEQUENCES
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                                                                   & Stevens, S.C.
Drive, Suite 401
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COMPUTER READBRE FORM:
CHEDIUM TYPE: Ploppy disk
CHEDIUM TYPE: Ploppy disk
COMPUTER: IDM PC Compatible
OPERATING SYSTEM: PP-OSS/MS-DOS
SOFTMARE: Petentin Release #1.0, Version #1.25
CORRENT APPLICATION NUMBER: US/08/222,177A
PLING DATE:
CLASSIFICATION NUMBER: US/08/222,177A
PLING DATE: 12.-DR-1869
ATTIONED APPLICATION NUMBER: US/08/222,177A
PRIOR APPLICATION NUMBER: US/08/222,177A
PRIOR APPLICATION NUMBER: US/08/222,177A
REGISTRATION NUMBER: US/08/222,177A
REGISTRATION NUMBER: US/08/222,177A
REGISTRATION NUMBER: US/08/222
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Gapop 60.0 , Gapext 60.0
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13847.741 Million cell updates/sec
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em_est5:*
em_est6:*
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em_est2:*
em_est3:*
                    em_est14 : * em_est15 : * em_est16 : * em_est16 : * em_est17 : * em_est18 : * em_es
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em_est28:*
em_est29:*
em_est30:*
em_est30:*
9b_est40:*
9b_est41:*
9b_est41:*
9b_est41:*
9b_est43:*
em_est31:*
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gb_est27:
gb_est28:
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em_est20:
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Minimum Maximum

Searched:

Run on:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

c 1 45 0.1 75 25 N68192 N68192 zailf07.sl	c 1 45 0.1 75 25 N68192	25	75	0.1	45	- 1	o ¦
Description	ID	BB	Length	Query	No. Score Match Length DB ID	Result	Res
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zallf07.sl Soares fetal
IMAGE:292261 3' similar
                                                                                                                                                                                                                                                                                        Unpublished (1995)
On Apr 14, 1993 this sequence version replaced Contact: Wilson RK
Washington University School of Medicine
                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammallis
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 75)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
                                       The WashU-Merck EST Project
                                                  Wilson, R.
                                                                                                                              Homo sapiens
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AA578401
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AA916300 nn22c08.s
AA983697 nn58f01.s
AA983697 nn58f01.s
N98204 0288C3 czap
C05051 C05051 Huma
AA548135 nx55a1.s
B80126 CIT-HS9-204
AF578401 n153c01.s
AQ276193 CITB1-E1-
AA5778401 n153c01.s
AA98778401 n153c01.s
AA9877847 n158690.s
AA019576 ze66h02.s
                     g1:503479
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AA078242 7H16G05 C
AA500598 vi90a02.r
B37890 HS-1046-A2-
R67088 yi30h05.s1
                                                                                                                                                                                                                                                                                                                                                         AA560791 v133b06.r
AQ025047 EP(2)1183
AI569475 tn87e04.x
AA289455 vb36d12.r
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AA752407 cn15d10.y
A1040422 Homo sapi
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B03985 cSRL-21b5-u
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D20989 HUMGS01971
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T25653 EST00522
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AA053038 z171e12.s
                                                                              Marra, M.,
                                                                                                                     Mammalia;
                                                                                                                                                                                                 clone
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                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
Contact: Ung-Jin Kim
CalTech Genome Research L
California Institute of T
Division of Biology, MS 1
Tel: 626 796 7066
Fax: 626 395 4901
                                                                                                                                                                                                                                                                                                                                                                                         1 Similarity
45; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: mis "*v vocation for 61.
High quality sequence stop: 61.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq.primer: ml3 -40 forward
Seq.primer: ml3 -40 forward
                                       end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                               Eukaryota; Metazoa;
Eutheria; Primates;
1 (bases 1 to 102)
                                                                                                                                                                                                                                                                   genomic survey sequence.
B62983
                                                                                                                                                                                                                                                                                     B62983 102 bp DI
CIT-HSP-669F15.TP CIT-HSP
                                                                             Email: ung@ash.tree.caltech.edu
Clones are available from Research
                                                                                                                                                                     Chromosomes
                                                                                                                                                                             Kim,U.-J., Adams,M.D. and Simon,M.I.
Determination of clone end sequences
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/db_xref="GDB:3800034"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
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/lab_host="DH10B (ampicillin resistant)"
  /organism="Homo sapiens"
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                             Location/Qualifiers
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b; Pred. No. 0.0
0; Mismatches
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Technology
147-75, Pasadena,
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                                                                              Genetics (info@resgen.com). BAC
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z171e12.s1 Stratagene colon (#937204) Homo sapiens CDNA clone
zMAGE:510094 3' similar to contains Alu repetitive element;, r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: estewatson.wustl.edu

Email: estewatson.wustl.edu

This clone is available royalty-free through LLNL; contact the

This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Chissoe, S., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMAGE Consortium (info@image.llnl.gov)
Seq primer: -40M13 fwd. from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On May 18, 1995 this sequence version Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Generation and analysis of 280,000 human expressed sequence tags Genome_Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
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//lab_host="Solr cells (kanamycin resistant)",
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//lab_host="Solr cells (kell) |
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                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
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0.0014;
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Query Match

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Score 44;

BB 27;

Length

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DEFINITION

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R18531 96
yf96e06.rl Soares
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wayne State University
5047 Gullen Mall, Detroit, MI 48202
Tel: 3135776708
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Center for Molecular Medicine and Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     An 'equalized cDNA library' by the reassociation of short double-stranded cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 93)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: msko@cmb.biosci.wayne.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KO, M.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     house mouse.
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                                                                                                                                                                                                                                                                                                          /note-"vector: pBluescript SK(-); Site_1: NotI; Site_2:
ECORI; mRNA was purified from the mouse Ltk- fibroblastoid
cultured cells. Double-stranded cDNAs were synthesized
from the mRNA using an ollgo(dT) NotI primer. After
shearing to 200-400 bp, a synthetic linker-primer, which
has one blunt and one sticky end and an internal EcoRI
site, was ligated to the cDNAs. The cDNAs were amplified
by the polymerase chain reaction (PCR) using the ligated
linker-primer sequence. After denaturation and
reassociation of the ds-cDNAs, and isolation of single-
stranded cDNAs by hydroxyapatite chromatography, the
single- stranded cDNAs were again amplified by PCR. The
cDNAs were digested with EcoRI and NotI, and inserted
into a plasmid vector."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93 bp mRNA EST 31-OCT-199 Equalized cDNA library from Ltk- cultured cells Mus cDNA cione A0001D11 3', mRNA sequence.
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cells"
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/clone="A0001D11"
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                                                                                                                                                                                    Score 43; DB 20;
Pred. No. 0.0057;
0; Mismatches 0
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Matches 42
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R18531.1
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 2194
Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL, contact the IMAGE Consortium (info@image.llnl.gov)
for further information. Putative full length read
Insert Length: 2194
Std Error: 0.00
                                                  sequence.
AA129957
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 96)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soarzes,M., Tan,F.,
Parsons,J., Rifkin,L., Rohlfing,T., Soarzes,M., Tan,F.,
                                                                             zn86h04.rl Stratagene lung
IMAGE:565111 5' similar to
                                                                                                                                                                                                                                 l Similarity
42; Conserv
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L1 repetitive element ;, r
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Homo sapiens
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Location/Qualifiers
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ilarity 100.0%;
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/db_xref="GDB:402738"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
/clone="IMAGE:30391"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Soares infant brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (1995)
                                                                                                        104 bp
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                                                                                                        mRNA
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                                                                             EST 27-NOV-1996 a 937218 Homo sapiens cDNA Alu repetitive element; r
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TGATCTTGGCTCACTGCAACCTCCGCCTCCTGGGTTCAAGC 90
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Hilller, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Chissoe, S., Dietrich, N., Kucaba, T., Lacy, M., Le, M., Le, N., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
Eutherla; Primates; Catarrhin1; Hominidae; Homo.

1 (bases 1 to 95)

1 (bases 1 to 95)

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2 (lases 1 to 95)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Res. 6 (9), 97044478
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Fax: 314 286 1810
Email: est@watson.wustl.edu
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Genome Res. 6 (9), 807–828 (1996)
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11; Conservative
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//lab_host="SOLR (kanamycin resistant)"
//note="Organ: lung; Vector: pBluescript SK-; Site_1:
//note="Organ: Lung; Vector: pBluescript Steel: Color of Lorent Steel: Lorent S
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/clone="IMAGE:565111"
/clone_1ib="Stratagene lung carcinoma 937218"
/tissue_type="lung carcinoma"
/cell_line="NCI_H69"
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/db_xref="GDB:4594175"
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Pred. No.
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Best Local S
Matches 40
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yc21f01.s1 Stratagene lung (#93/210
TMAGE: 81337 3' similar to contains
                                                                                                                                                                                                                                                                                   Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chiasoe, S., Dietrich, N., DuBugue, T., Favello, A., Gish, W., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Riikin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40;
Email: est@watson.wustl.edu
Insert Size: 513
Insert Size: 513
High qality sequence stops: 69 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seg primer: -40ml3 fwd. ET from Amersham.
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Fax: 314 286 1810
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On Nov 6, 1997 this sequence version replaced
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 105)
                                                                                                                                              Washington University School of Medicine
                                                                                                                                                                                                                                Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807–828 (1996)
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314 286 1810
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/lab_host="SOLR cells (kanamycin resistant)"
/lab_host="SOLR cells (kanamycin resistant)"
/note="organ: ovary; Vector: Bluescript SK; Site_1: EcoRI.
Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dT.
Total ovary; tissue, normal, caucasian. Average insert
size: 0.8 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5'
GAATTCGGCACGAG 3' -3' adaptor sequence: 5'
GACTCGAGTTTTTTTTTTTTTTTTT 3'"

CTCGAGTTTTTTTTTTTTTTTTT 3'
a. 30 c. 24 g. 26 t.
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/clone_lib="Stratagene ovary (#937217)"
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/db_xref="taxon:9606"
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similar to
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On May 5, 1995 this sequence version replaced g1:797742.
On May 5, 1995 this sequence version replaced g1:797742.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert Strausberg@nih.gov
Email: Robert Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40;
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                                                                                                                                                             High quality sequence stop:
                                                                                                                                                                                                                                                                                       cDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-GGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                Tissue Procurement: Chri. Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumor Gene Index
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National Cancer Institute, Cancer Genome Anat
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1557422"
/clone_lib="NCI_CGAP_Lu5"
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/clone="IMAGE:81337"
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/db_xref="GDB:484954"
                         /tissue_type="carcinoid"
/lab_host="DH10B"
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      lung; Vector:
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(Pharmacia) with

Sequencing Center information can be

Michael

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Insert Length: 513
Seq primer: -21m13
                        /clone_lib="Stratagene lung (#937210)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
On Apr 14, 1993 this sequence version replaced gi:692709
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1 (bases 1 to 101)
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H1gh quality sequence stop: 93.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA Library Preparation: Stratagene, Inc. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tissue Procurement: L. Jeffrey Medeiros, M.D., Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1088107"
                                                                                                                                                                                                                       /tissue_type="kidney tumor"
/lab_host="SOLR (kanamycin resistant)"
                                                                                                                                                                                                                                                           'sex="mixed"
                                                                                                                                                                                                                                                                                clone_lib="NCI_CGAP_Kid6"
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    DB 35;
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                    Length 101;
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                                      C05051 Hum
C05051 Hum
3NHC4544,
C05051
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Tel: 407 384 2061
Fax: 407 384 3095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Debopam Chakrabarti
Department of Molecular Biology and Microbiology
University of Central Florida
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0288C3 czapPFDd2.1, I
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                                                                               Human heart cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dchak@pegasus.cc.ucf.edu
                                                                                                                                                                                                                                                                                                                                                                                              using an oligo dT-Xho I primer. Second strand was prepared using RNase H and DNA polymerase I. EcoR I adapters were ligated to the cDNA, and it was digested with Xho I. Prepared fragments were ligated into EcoR I Xho I digested lambda ZAP II vector. "

3 1 t 4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_llb="czapPFDd2.1, Debopam Chakrabarti"
/lab_host="E. coli XL-1 blue"
/note="Vector: Lambda ZAP II; Site_1: EcoR I; Site_2: Xho
I; PolyA+ RNA, from asynchronous blood stage parasites of
I; PolyA+ RNA, from asynchronous blood stage transcribed
the Dd2 isolate cultured in vitro, was reverse transcribed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:5833"
/clone="PF0288C"
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                                                       mRNA sequence.
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Debopam Chakrabarti Plasmodium falciparum
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                                                                                        Tumor Gene Index
Unpublished (1997)
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1397885.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: David G. Bostwick, M.D., Rodrigo F. Chuaqui,
M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Mashington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA548135 92 bp
nk55all.sl NCI_CGAP_Pr7
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Tel: 81-3-5449-5372
Eukaryota; Metazoa; Chordata; Craniata; Vertebra Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 92)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence.
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                                                                                                                                                                                                                                                                                                                                            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                             www-bio.llnl.gov/bbrp/image/image.html
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Location/Qualifiers
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/clone_lib="Human heart cDNA (YNakamura)"
/dev_stage="adult"
/note="Organ: heart; normalized directionally cloned cDNA from adult heart"
26 c 37 g 17 t
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                               Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0208
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Building (1998)
Unpublished (1998)
Other_GSSs: CIT-HSP-2042J24.TF
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Use of a random BAC End Sequence Database for Sequence-Ready Map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CIT-HSP-2042J24.TR CIT-HSP
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                                                                                                                                                                                                                                                                                                        Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                 Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                   Email: mdadams@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Mark Adams
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1017404"
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                                                                                   /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                         /organism="Homo sapiens"
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/lab_host="DH10B"
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                                                                                                                                                        'clone_lib="CIT-HSP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seg primer: M13RP1
High quality sequence stop: 70.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
Insert Size: 614
High quality sequence stops: 70 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE. Consortium (info@image.llnl.gov) for further information.
Insert Length: 614 Std Error: 0.00
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Generation and analysis of 280,000 human expressed sequence tags genome Res. 6 (9), 807-828 (1996) 97044478
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1 (bases 1 to 105)
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ye35b02.rl Stratagene lung (#937210) Homo sapiens cDNA clone
IMAGE:119691 5' similar to contains Alu repetitive element;, mRNA
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                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="GDB:487980"
/db_xref="taxon:9606"
/clone="IMAGE:119691"
                                                                                                                                                                                                                                                                                             /dev_stage="72 years"
/lab_host="SOLR cells (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                    'clone_lib="Stratagene lung (#937210)"
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Title: Perfect score:

Scoring table: Sequence:

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Minimum DB Maximum DB

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Patent: US 5582979-A 244 10-DEC-1996;
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Homo sapiens 4000 year old i
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Eutheria; Primates; Catarrhini;
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/chromosome="12"
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Sequence 65 from patent US
I31153
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Ancient DNA: extraction, characterization, molecular cloning, enzymatic amplification
Proc. Natl. Acad. Sci. U.S.A. 86 (6), 1939-1943 (1989)
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Similarity 100.0%; Pred. No. 4.2e-10;
43; Conservative 0; Mismatches 0;
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                                                                                                    unclassified.

1 (bases 1 to 85)

Jeffreys,A.J. and Armour,J.

IDENTIFICATION OF SIMPLE TANDEM REPEATS
PAtent: WO 9517522-A 44 29-JUN-1995;
UNIV LEICESTER (GB)
Other publication AU 1277995 950710.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 40)

Resnick, M.A., Larionov, V.L., Kouprina, N.Y. and TRANSFORMATION-ASSOCIATED RECOMBINATION CLONING PATENT: WO 9801573-A 15-JAN-1998;
US HEALTH (US)
                                                                                                                                                                                                                                                                                                                                                                                                  Ch 0.1%; Score 40; DB 5; L6 1 Similarity 100.0%; Pred. No. 1.4e-08; 40; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                             A45374 85 bp DNA
Sequence 44 from Patent WO9517522.
A45374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A68621 40 bp DNA
Sequence 1 from Patent WO9801573.
A68621 G1:4759648
                                                                                                                                                                                                              unidentified
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/organism="unknown"
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/db_xref="taxon:32644"
12 c 13 g
                                                                          /db_xref="taxon:32644"
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Sequence 44 from p
AR061179
AR061179.1 GI:59
                                                                                                                                         Armour, J.A.L.
Armour, J.A.L.
Direct Submission
Submitted (04-MAY-1995) J.A.L. Armour, University
Submitted (04-MAY-1995) J.A.L. Armour, University
Dept of Genetics, University Road, Leicester LE1 7
Dept Location/Qualifiers
                                                                                                                                                                                                                                                                                                                  H.sapiens simple tandem X86915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 85)
Jeffreys, A. John and Armour, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unknown.
Unclassified.
                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Vertebrata; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 85)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Simple tandem repeats Patent: US 5843647-A 44 01-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unknown
                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                    Armour, J.A.L., Swallow, J.,
                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                          human .
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1 c 24 g
                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="19"
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                                                                    /rpt_type=TANDEM
1 c 24 g
                                                                                                            /clone="wg3b10"
                                                                                         'note="simple tandem repeats"
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Sequence
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1 (bases 1 to 60)
de la Monte, S. and Wands, J.R.
Human alpha-galactosidase M36133 M36133.1 GI:179543
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                                                                                                                                                                                                                                               de la Monte, S. and Wands, J.R. Neural thread protein gene expression
                                                                                                                                                                                                                                                                   Unclassified.
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14 c 15 g
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Best Local Similarity 100.
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Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 36; Conservative 0; Mismatches 0;
gene
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                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 101)
Bernard,O.A., Romana,S.P., Schichman,S.A., Mauchauffe,M.,
Jonveaux,P. and Berger,R.
Jonveaux,P. and Berger,R.
Partial duplication of HRX in acute leukemia with trisomy 11
Leukemia 9 (9), 1487-1490 (1995)
95387660
                                                                                                                                                                                                                                                                            GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 170933] from the original journal article. This sequence comes from Fig. 3.
Map location: 11q23.
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J. Biol. Chem. 265, 9319-9326 (1990)
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Kornreich,R, Bishop,D.F. and Desnick,R.J.
Alpha-galactosidase A gene rearrangements causing Fabry disease:
Identification of short direct repeats at breakpoints in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.
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28 c 17 g 1:
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100.0%; Pred. No. 1.4e-06;
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Search completed: April 1, 2000, 01:57:28 Job time: 253997 sec

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12517.949 Million cell updates/sec
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   GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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Q33855
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T65770
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Q24810
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Q33618
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T65740
T66081
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pSPORT-La syntheti
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PCR amplification
Microsatellite seq
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Repeat sequence fr
(dC-dA)n.(dG-dT)n
Repeat sequence fr
Repeat sequence fr
Microsatellite seq
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Microsatellite seq
Microsatellite seq
                                                                                                                                                                                                                                                                                                     Description
                                                                                                                          PCR amplification Inter-Alu specific
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RESULT T65740 ID T6 AC T6 DT 17 DE Re KW PC

765740 standard; DNA; 91 BP.
765740;
17-JUN-1997 (first entry)
Repeat sequence from polymorphic marker clone Mfd39.
Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree;

B 8

Matches

54;

Conservative

0

Mismatches

0;

Indels

0

Gaps

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Query Match Best Local	05-SEP-11 06-SEP-11 (MARS-) R (MARS-) R Weber JL, Weber JL, WPI: 97-0 Detection (dC-dA)n Disclosu The inver having ti markers. repeats, human dse containit containit chromosor probe. were amp yerence sequence sequence	JLT 1 762 765762; 765762; 765762; 17-JUN- Repeat PCR; po 11nkage hybridi Homo sa US55829 11-DEC- 21-APR-	00000044444444400000000000000000000000
Simi	July 1, 1994; 1994	standar 1997 (sequenc phism; lymeras lymeras lyanalys Isation; 1991-A. 1996.	& & & & & & & & & & & & & & & & & & &
similarity	991; US-75435 991; US-72217 MARSHFIELD CL ; 042299/04. n of polymorp (dG-dT)n - us re; Column 11 ntion relates he sequence (Primers bas especially f netic analysi al animal or ng the repeat me-specific p over 100 repe lified by pri has been det having the f 60 BP;	OLT 1 762 762 762 762 762 762 762 762 762 76	000000000000
0.29	CLINIC. CLI	E 60 B pntry) polym polym seque seque i reac petic psome;	70 1 70 1 73 1 33 1 33 1 34 1
0%; Score 54; DB 1; Length	R 05-SEP-1991; US-754351. R 04-APR-1994; US-222177. R 04-APR-1994; US-222	ALIGNMENTS 60 BP. 60 BP. polymorphic marker clone Mfd67. sequence; genetic marker; primer; ampli reaction; paternity; maternity; human; etic disease; animal; plant; breeding; some; ds.	Q34053 Q34155 Q34155 Q34146 Q34140 Q34140 Q34009 Q3400 Q
1 60;	primers repeat sequences sed as genetic ed to detect these enity testing, metic disease, /sis. Clones ridisation of poly(GC-dA). (GG-dT) serts from the clones swhere the repeat . This repeat s the repeat	c; amplification; human; pedigree; seding; locus;	Poly GT enhancer e Microsatellite seq Sequence of a micr Sequence of a micr Sequence of a micr Alicrosatellite seq Allelic ladder, DI Microsatellite seq Sequence of a micr Repeat sequence fr Repeat sequence fr Microsatellite seq

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RESULT
T66081
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DR Detection of polymorphic genetic markers of the form PT (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers PT (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers PT (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers PT (dC-dA)n(dG-dT)n + using novel nucleic acid mols. as primers PT (dC-dA)n. (dG-dT)n which can be used as genetic CC the invention relates to the isolation of polymorphic repeat sequences CC markers. Primers based on these sequences can be used to detect these CC commercial animal or plant breeding or paternity or maternity testing. CC containing the repeat sequences were isolated by hybridisation of CC chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) CC composed the contained are shown in T65704-797. This repeat CC were amplified by primers T65798-T66047. Those clones where the repeat CC sequence has been determined are shown in T65704-797. This repeat CC sequence is from the formula: (TC)12.5GTT(TC)11.5(CA)14A(CA)5.5.
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Best Local S
Matches 50
                                                                                                                                                                                                                                                                                                  21-APR-1989; 341562.
21-APR-1989; US-341562.
05-SEP-1991; US-754351.
04-APR-1994; US-222177.
(MARS-) MARSHFIELD CLINIC.
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21-APR-1989; 341562.
21-APR-1989; US-341562.
05-SEP-1991; US-754351.
04-APR-1994; US-222177.
WPI; 97-042299/04.

WPI; 97-042299/04.

Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers Example 8; Column 57-58; 186pp; English.

The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n. (dG-dT)n which can be used to detect these markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis.

The repeats, when analysed, fall into 4 categories:

1) perfect repeats which are alternating tandem CA repeats with no interruptions and without adjacent repeats of another sequence;

2) imperfect repeats which are defined as 2 or more runs of uninterrupted
                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
US5582979-A.
10-DEC-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-JUN-1997 (first entry)
(dC-dA)n.(dG-dT)n polymorphic repeat sequence #12.
(dC-dA)n.(dG-dT)n polymorphic repeat sequence; genetic marker; primer; amplification; Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T66081;
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                                                                                                                                                                                                                                                                                      Weber
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50; Conserv
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Pred. No.
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RESULT T65791

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<u>ب</u>

42

Matches Query Match Best Local

42;

Conservative

0;

Score 42; DB Pred. No. 0.0 0; Mismatches

DB 1; L 0.00012;

Length

Indels

0

Gaps

0

Similarity

0.1%;

ΑIJ

T65791 standard; DNA; T65791;

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problements of the form primers (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers Claim 1; Column 9-10; 186pp; English.

Claim 1; Column 9-10; 186pp; English.

The invention relates to the isolation of polymorphic repeat sequences having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) cprobe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers T65798-T66047. Those clones where the repeat sequence has been determined are shown in T65704-797. This repeat sequence is from the marker clone Mdf5 which contains the repeat sequence as from the marker clone Mdf5 which contains the repeat sequence having the formula: (CT)7(CA)23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local (
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10-DEC-1996.
21-APR-1989; 341562.
21-APR-1989; US-341562.
05-SEP-1991; US-754351.
04-APR-1994; US-222177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 JUN-1997 (first entry)

Repeat sequence from polymorphic marker clone Mfd5.

Repeat sequence from polymorphic marker; primer; amplification; polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CA repeats separated by no more than 3 consecutive non-repeat bases;
3) compound perfect repeats which are uninterrupted runs of CA separated by no more than 3 consecutive non-repeat bases from a run of at least 5 uninterrupted dinucleotide or longer repeats of a sequence other than (dC-dA)n.(dG-dT)n, or from at least 10 uninterrupted mononucleotides; and 4) imperfect compound repeats which are defined as for the perfect compound repeats which are defined as for the perfect rhis sequence is an example of a compound imperfect repeat sequence of structure: T(CT)_12GTT_T(C)_11T(CA)_14(AC)6.

Sequence 92 BP; 21 A; 43 C; 1 G; 27 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T65707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hybridisation; chromosome; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                        WPI; 97-042299/04.
                                                                                                                                                                                                                                                                                                                                                                                              Weber
                                                                                                                                                                                                                                                                                                                                                                                                               (MARS-) MARSHFIELD CLINIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard; DNA; 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 100
50; Conservative
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Pred. No.
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2.9e-07;
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Detection of polymorphic genetic markers of the form
Pr (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as primers
Claim 1; Column 13-14; 186pp; English.

The invention relates to the isolation of polymorphic repeat sequences
The invention relates to the isolation of polymorphic repeat sequences
C markers. Primers based on these sequences can be used to detect these
C repeats, especially for use in e.g paternity or maternity testing,
C human genetic analysis such as linkage analysis of genetic disease,
C containing the repeat sequences were isolated by hybridisation of
C chromosome-specific phage libraries with a synthetic poly(dC-dA).(dG-dT)
C probe. Over 100 repeat blocks were isolated. The inserts from the clones
C were amplified by primers T65798-T66047. Those clones where the repeat
C sequence has been determined are shown in T65704-797. This repeat
C sequence is from the marker clone Mdf120 which contains the repeat
C Sequence 50 BP; 20 A; 25 C; 0 G; 5 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
Polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding gene mapping, and selective breeding Table 7; Page 170; 517pp; English.

The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence used to generate the required PCR primers for in vitro
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Q33603
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21-APR-1989; US-341562.
05-SEP-1991; US-754351.
04-APR-1994; US-222177.
                                                                                                                                                                                                                                                 (GENM-) GENMARK.
Georges M, Massey JM;
WPI; 92-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                 02-FEB-1993 (first entry)
Microsatellite sequence from clone AGLA296.
PCR; selection; primers; OPTIPRIM; breeding;
genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3945
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-JUN-1997 (first entry)
Repeat sequence from polymorphic marker clone Mfd120.
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                                                                                                                                                                                                                                                                                                       15-JAN-1992; U00340.
15-JAN-1991; US-642342.
                                                                                                                                                                                                                                                                                                                                            06-AUG-1992.
                                                                                                                                                                                                                                                                                                                                                              WO9213102-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; DNA; 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; L
0.00025;
                                                                                                                                                                                                                                                                                                                                                                                                                     cattle; parentage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amplification;
numan; pedigree;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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RESULT 8
Q33594/C
ID Q33594; standard; DNA; 6
AC Q33594;
DT 02-FEB-1993 (first ent
DE Microsatellite sequence
KW PCR; selection; primers
KW genetic mapping; traits
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                                                                                                                                                                                                                                                                                                                                                            PI Georges M, Massey JM;

PR Holymorphic bovine DNA markers - used in genetic identification,

PR Polymorphic bovine DNA markers - used in genetic identification,

PR Polymorphic bovine DNA markers - used in genetic identification,

PR page 241; 517pp; English.

Cr hable 7; Page 241; 517pp; English.

Cr he sequence is that of a bovine microsatellite sequence obtd. by

Cr screening a library of bovine MboI DNA fragments of between

Cr one out of 50 clones cross-hybridised. Assuming independent

Cr one out of 50 clones cross-hybridised. Assuming independent

Cr one out of 50 clones cross-hybridised. Assuming independent

Cr one out of 50 clones cross-hybridised. Assuming independent

Cr one out of 50 clones cross-hybridised. Assuming independent

Cr one out of 50 clones cross-hybridised. Assuming independent

Cr one out of 50 clones cross-hybridised.

Cr one out of 50 clones information for ca. 230 such bovine microsatellites

Cr is summarised in the specification and indexed herein (see below).

Cr is sequences upstream and downstream of the microsatellites

Cr is summarised in the specification and indexed herein (see below).

Cr amplification of the corresp. microsatellite (using the program of completing in the program of completing in cattle, to allow selective breading.

Cr or parentage testing, and in the genetic mapping of economic trait cr of contraits contraits esp. in cattle, to allow selective breading.

Sequence 62 BP; 22 A; 0 C; 31 G; 9 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 41
                                                                                                                                                                                                                                                                                         Query Match
Best Local (
                                                                                                                                                                                                                                                                         Matches
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033779
033779
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                                                                                                                                                                                                                amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding.

See also 033501-34437.

Sequence 56 BP; 19 A; 0 C; 28 G; 9 T;
   02-FEB-1993 (first entry)
Microsatellite sequence from clone AGLA29.
PCR; selection; primers; OPTIFRIM; breeding;
genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-AUG-1992.
15-JAN-1992; U00340.
15-JAN-1991; US-642342.
(GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Microsatellite sequence from clone TGLA182. PCR; selection; primers; OPTIPRIM; breeding; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genetic mapping;
Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41
                                                                                                                                                                                                41 CTCTCTCTCTCTCTCTCTCACACACACACACACACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; DNA;
                                                                                                                                                                                                                                                                         41;
                                                                                                                                                                                                                                                                                             Similarity
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Similarity 100.0%;
41; Conservative
                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                           0.1%;
                                                                                                   63
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                                                                                                                                                                                                                                                                                           Score 41;
Pred. No.
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0.00024;
0;
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Eg 0.0
                                                                                                                                                                                                                                                                                             .00024;
                       cattle; parentage;
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                                                                                                                                                                                                                                                                                                               Length 62;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           parentage;
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PS Table 7; Page 167; 517pp; English.

CC The sequence is that of a bovine microsatellite sequence obtd. by
CC Screening a library of bovine MboI DNA fragments of between
CC One out of 50 clones cross-hybridised. Assuming independent
CC One out of 50 clones cross-hybridised. Assuming independent
CC One out of 50 clones cross-hybridised. Assuming independent
CC (T6)n >9 microsatellites in the bovine genome is estimated at >100,
CC on the sequence information for ca. 230 such bovine microsatellites
CC is summarised in the specification and indexed herein (see below).
CC The sequences upstream and downstream of the microsatellite sequence
CC amplification of the corresp. microsatellite (using the program
CC OPTIFRIM). The microsatellites may be used to identify individuals,
CC for parentage testing, and in the genetic mapping of economic trait
CC loci, or genes involved the determinism of economically important
CC see also Q33501-34437.
CS Sequence 63 BP; 22 A; 0 C; 32 G; 9 T;
PT gene mapping, and selective breeding
Table 7; Page 176; 517pp; English.

Table 7; Page 176; 517pp; English.

The sequence is that of a bovine microsatellite sequence obtd. by
CC Screening a library of bovine MboI DNA fragments of between
CC One out of 50 clones cross-hybridised. Assuming independent
CC One out of 50 clones cross-hybridised. Assuming independent
CC One out of 50 clones cross-hybridised. Assuming independent
CC ONE of microsatellites in the bovine genome is estimated at >100,
CC ONE of microsatellites in the bovine genome is estimated at >100,
CC ONE of microsatellites in the bovine bovine microsatellites
CC OS summarised in the specification and indexed herein (see below).
CC The sequences upstream and downstream of the microsatellite sequence
CC were used to generate the required PCR primers for in vitro
CC amplification of the corresp. microsatellite (using the program
CC mapping of testing, and in the genetic mapping of economic trait
CC for parentage testing, and in the genetic mapping of economic trait
CC traits esp. in cattle, to allow selective breeding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENM-) GENMARK.
Georges M, Massey
WPI; 92-284684/34.
                                                                                                                                                                                                                                                                                                                                               Georges M, Massey JM;
WPI; 92-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                   15-JAN-1992;
15-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genetic mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Microsatellite sequence from clone AGLA8.
PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q33618 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JAN-1992;
15-JAN-1991;
                                                                                                                                                                                                                                                                                                                           Polymorphic bovine DNA markers -
                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9213102-A.
06-AUG-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-FEB-1993 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                    (GENM-) GENMARK.
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les 41; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                   US-642342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              traits; amplification; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                         used in genetic identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
3. 0.00024;
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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RESULT 10
V19044/c
ID V19044
     ID ACC DT COS OS OS OF PROPERTY OF PROPERT
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Best Local S
Matches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                              29-JUN-1995.
21-DEC-1994; G02789.
21-DEC-1993; GB-026052.
(UYLE-) UNIV LEICESTER.
Armour J, Jeffreys AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24755 TCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           recombination using vector comprising yeast centromere, marker, yeast telomere and nucleic acid for recombination

Example 1; Page 45; 117pp; English.

This is the nucleotide sequence for the PCR primer used in the amplification of the Alu repeat sequence, which is used to demonstrate the processes described in the invention. It involves the creation and use of circular yeast artificial chromosome (YAC) to selectively clone specific nucleic acids from a background of mixed nucleic acids by introducing the vector(s) into E. coli cells. They can be used to rapidly isolate human DNA where only a part of the sequence of DNA is known. Using the methods large fragments of DNA can be easily cloned and analysed.

Sequence 40 BP; 7 A; 12 C; 13 G; 8 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    See also
Sequence
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09-JUL-1996; U11478.
09-JUL-1996; WO-U11478.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
KOUDFINA NY, LARIONOV VL, PERKINS EL, RE
WPI; 98-110234/10.
                                                                                                                                                                                                                                                                        Simple tandem repeat; STR;
                                                                                                                                                                                                                                                                                                                                                     Q95218 standard; DNA; Q95218;
                                                                                                                                                                                                                      second
                                                                                                                                                                                                                                                characterisation; mapping;
                                                                                                                                                                                                                                                                                                                           08-FEB-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Preparation of yeast artificial chromosomes -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces sp. WO9801573-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCR; primer; amplification; Alu repeat sequence; vector; circular yeast artificial chromosome; YAC; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 V19044;
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                            95-240682/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCGGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACC 1
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                                                                                                                                                                                                                         part; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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40 BP; 11
  simple tandem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.1%;
                                                                                                                                                                                                                                                                                                                                                                               85
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0;
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repeat
                                                                                                                                                                                                                                                   corresponding to the 2nd part wg3b10; treatment; genetic; di linkage studies; analysis; all
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Pred. No. 0.00055;
0; Mismatches 0;
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  DNA - by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a 1; L
.00055;
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05-MAR-1992; U06119.
27-AUG-1991; U05119.
27-AUG-1999; US-573570.
(UYRO) ROCKEFELLER UNIV.
(UYVE) UNIV OF VERMONT.
Heintz N, Heintz NH, Dailey LA, C:
WPI; 92-096839/12.
                                                                                                                                     11815 CTCTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTTCTTT 11854
                                                                                                                                                                                                                                                              Viral infection and cancer

Example 2: Page 42: 82pp; English.

Competition experiments using the DNAseI protection assay showed that an oligonucleotide contg. 15 tandem ATT repeats was an effective competitor for binding of the HeLa factor. This oligo was used to prepare an oligonucleotide affinity column for purification of RIP60 from Chinese hamster cells. The protein recognises and binds to an (ATT)n motif in the dhfr gene ori. It can also bind to the yeast ARS1 domain B. See Q22753 and Q24811.

Sequence 63 BP; 19 A; 5 C; 6 G; 33 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       095218 is a simple tandem repeat (STR) corresponding to the 21 of wg3b10. The STR can be used for treatment and diagnosis in and veterinary medicine, partic. for genetic characterisation mapping, linkage studies and analysis/diagnosis of acquired dialleles.
   Q71808 standard;
Q71808;
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DNA footprinting; (ATT)n binding
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and rescreening,
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New biocompatible medical devices and articles acid-glycolic acid polyester in which monomer u individually and specifically determined Example 2; Page 53; 67pp; English.

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Pred. No. 0.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clips;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 0.1
Best Local Similarity 100.
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New biocompatible medical devices and articles - using a lactic acid-glycolic acid polyester in which monomer units are individually and specifically determined

Example 1; Page 45; 67pp; English.

This sequence represents a fragment of the plasmid psporT Ic which contains the 5' fragment of the synthetic genes which encode polyesters, given in Q71801-02, under the control of the E. coli trpA transcription initiator and followed by FokI and HindIII restriction sites. A further fragment of the synthetic genes were ligated into psporT Ic to give plasmid psporT Id (see also Q71810-11), with the final fragment being inserted in a third round of ligation to give psporT Ie (see also Q71812).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pSPORT-IC synthetic polyester gene 5' fragment and trpA initiator. Synthetic gene; synthesis; polyester; a-amino acid analogue; clips; stop codon; stop signal; monomer unit; lactate; glycolate; staples; translation initiation; modified; Met-tRNAf; cyanogen bromide; pins; co-polymer; sutures; drug delivery device; screws; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          first position of the polymer chain. The resulting power the Met. Co-polymers manner may be used to produce sutures, staples, clips, devices, pins and screws.

Sequence 81 BP; 47 A; 6 C; 4 G; 24 T;
                                                                                                                                                                                                                                                                                               01-JUL-1994.
31-DEC-1993; 112716.
31-DEC-1992; US-999520.
                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_signal
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                                                                                                                                                                                                                                          WPI; 94-272324/34.
                                                                                                                                                                                                                                                           (USSU ) US SURGICAL CORP. Gruskin EA;
                                                                                                                                                                                                                                                                                                                                                               CA2112716-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
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19. .21
                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Start codon" 22. .93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                /*tag= c
/note= "Polyester gene 5' fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "trpA initiator"
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0; Mismatches
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hes 0;
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so Q71812-
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CC length sequences given in Q71801-02 in an E. coli cell free medium. The CC length sequences given in Q71801-02 in an E. coli cell free medium. The CC expressed sequences represent synthetic genes which were used in the CC synthesis of polyesters derived from the a-amino acid analogues of an CC amino acid except pro. Of the three stop codons, UAA, UAG and UGA, one CC of these stop codons is reversed for the stop signal for the monomer CC units of the polyester. Lactate and glycolate are encoded by UAA and CC UAG, respectively. Initiation of translation always starts at an AUG codon, therefore the first lactate of the chain may be encoded by an AUG codon. This is accomplished through the use of a specially modified the tis incorporated in the first position of the polymer chain. The CC met is incorporated in the first position of the polymer chain. The cresulting polymer is treated with cyanogen bromide to remove the Met. CC cpolymers produced in this manner may be used to produce sutures, Staples, clips, drug delivery devices, pins and screws.

Sequence 103 Bp; 58 A; 7 C; 9 G; 29 T;
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Query Match Q.1%; Score 39; DB 1; Length 103;
Best Local Similarity 100.0%; Pred. No. 0.00093;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Mismatches 10; Misma

Db 23 AATAATAATAATAATAATAATAATAATAATAATAAT

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Search completed: April 1, 2000, 04:18:02 Job time: 260880 sec

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Minimum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
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Match
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1 GTATATATCATGTGTACTTG
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                       GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/5C_COMB.seq:*
/cgn2_6/ptodata/1/ina/5D_COMB.seq:*
/cgn2_6/ptodata/1/ina/5D_COMB.seq:*
/cgn2_6/ptodata/1/ina/6COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-08-222-177A-430
US-08-222-177A-430
US-08-222-177A-39
US-08-222-177A-39
US-08-322-766A-44
US-08-454-557C-57
US-08-450-673C-69
US-08-450-673C-69
US-08-450-673C-69
US-08-450-673C-69
US-08-450-673C-92
US-08-450-673C-92
US-08-450-577-17A-972
US-08-222-177A-715
US-08-222-177A-717
US-08-459-222-177A-317
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                                            US-08-267-803B-45
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                Sequence 244, App
Sequence 106, App
Sequence 430, App
Sequence 379, Appl
Sequence 57, Appl
Sequence 57, Appl
Sequence 57, Appl
Sequence 57, Appl
Sequence 59, Appl
Sequence 69, Appl
Sequence 69, Appl
Sequence 92, Appl
Sequence 312, App
Sequence 317, App
Sequence 318, App
Sequence 317, App
Sequence 31
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                     Patent
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Query Match
                                                                                                                                                        TOPOLOGY:
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ALIGNMENTS	US-08-222-177A-183	US-08-222-177A-74	US-08-222-177A-403	US-08-222-177A-400	US-08-222-177A-119	US-08-222-177A-137	US-08-222-177A-397	US-08-222-177A-198	US-08-222-177A-140	US-08-222-177A-358	US-08-222-177A-104	US-08-222-177A-189	US-08-222-177A-77	US-08-222-177A-322	US-08-222-177A-192	US-08-222-177A-180	US-08-222-177A-172	US-08-222-177A-110	US-08-222-177A-218
		Sequence 74, Appl	Sequence 403, App	Sequence 400, App		Sequence 137, App	Sequence 397, App	Sequence 198, App	Sequence 140, App	Sequence 358, App	Sequence 104, App	Sequence 189, App				Sequence 180, App			

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FILING DATE.

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/341,562

FILING DATE: 21-APR-1989

ATTORNEY/AGENT INFORMATION:

NAME: Sara, Charles S.

REGISTRATION NUMBER: 30,492

REFERENCE/DOCKET NUMBER: 09855.601

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION 1870-2106
MOLECULE TYPE: DI
MMEDIATE SOURCE:
CLONE: mfd67rs
US-08-222-177A-244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 60 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244, Application US/08222177A
o. 5582979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRY: USA
53717-1914
                                                                                                                             nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: DeWitt Ross & Stevens, S.C.
8000 Excelsior Drive, Suite 401
                                                                                       linear
                                                              DNA (genomic)
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0.2%;

Score 54;

DB 1;

Length 60;

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; TOPOLOGY: linea;
; MOLECULE TYPE: DN:
; IMMEDIATE SOURCE:
; CLONE: mfd39rs
US-08-222-177A-166
                             US-08-222-177A-430
Sequence 430, Application US/08222177A
Patent NO. 5582979
GENERAL INFORMATION:
APPLICANT: Weber, James L.
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Best Local Similarity
Matches 50; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.0%; Matches 54; Conservative 0;
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 91 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 53717-1914

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                 REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (608) 831-2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IITLE OF INVENTION: LENGTH POLYMORPHISMS IN ITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES 460
    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Sara, Charles S. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Madison
STATE: Wiscons
                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (608) 831-2106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wisconsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3: DeWitt Ross & Stevens, S.C. 8000 Excelsior Drive, Suite 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/08222177A
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                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                           DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                        double
                                                                                                                                                                                                                       0.2%;
LENGTH POLYMORPHISMS IN (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US 07/341,562
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                                                                                                                                                                                                                         Score 50;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pred. No. 5.9e-09;
; Mismatches 0;
                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                       DB 1; L
. 1.1e-07;
                                                                                                                                                                                                           0
                                                                                                                                                                                                                                   Length 91;
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Best Local S
Matches 50
                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                          CIII.
STATE: WLL
COUNTRY USA
TTD: 53717-1914
TEADABLE F
     CLASSIFICATION: 435
PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
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                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                             APPLICANT: Weber,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
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Sequence 65, Application US/08222177A Patent No. 5582979
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FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 0986
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 92 base pairs
TYPE: nucleic acid
                                     SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: DeWitt Ross & Stevens, S.C.
STREET: 8000 Excelsior Drive, Suite 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
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SOFTWARE: Patentin Release #1.0, Version #1
APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
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8000 Excelsior Drive, Suite 401
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100.0%; Pred. No. 1.
1ve 0; Mismatches
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                     US/08/222,177A
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US-08-222-177A-379

; Sequence 379, Application US/08222177A

; Patent No. 5582979
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                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UDATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY_AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
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NAME: SAIR, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 0980
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 53717-1914

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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IMMEDIATE SOURCE:
CLONE: mfd5rs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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mes 42; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (608) 831-2106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/341,562 FILING DATE: 21-APR-1989
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                  STRANDEDNESS:
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                                                 ENGTH:
                                  nucleic acid
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                                                 50 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: DeWitt Ross & Stevens, S.C.
8000 Excelsior Drive, Suite 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Weber, James L.

VENTION: LENGTH POLYMORPHISMS IN

VENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
                                                                                                                  (608) 831-2106
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   linear
                                                                                                                                   (808)
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                                                                                                                                  831-2100
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100.0%; Pred. No
tive 0; Mismat
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      RESULT /
US-08-454-557C-57
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Sequence 57, Application US/08454557C
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US-08-332-766A-44/c
; Sequence 44, Application US/08332766A
; Patent No. 5843647
; GENERAL INFORMATION:
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; IMMEDIATE SOURCE:
; CLONE: mfd120rs
US-08-222-177A-379
                                                                                                                                ; TOPOLOGY: linear; MOLECULE TYPE: DNA (genomic) US-08-332-766A-44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
"hes 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                        Query Match
Best Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/332,766A
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9326052.9
FILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                    TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
               SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (202) 861-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: JEFFREYS, APPLICANT: ARMOUR, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                  NAME: BIRD, Donald J. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                NAME:
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                                                                                                                                                                                         nucleic acid
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                                                                                                                                                                                                          85 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U.S.A.
                                                        Conservative
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                                                                                                                                                                            single
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                                                                      0.1%; Score 40;
100.0%; Pred. No.
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                                                          Mismatches
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                                                                                    DB 3;
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Best Local Similarity
Watches 37; Conserve
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Patent No. 5948634
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APPLICANT: de la Monte, S
APPLICANT: Wands, Jack R.
                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08
FILING DATE: 30-MAX-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ITILE OF INVENTION: Neural Thread Protein Gene Expression and Detection
ITILE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection ITILE OF INVENTION: of Alzheimer's Disease NUMBER OF SEQUENCES: 121
                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                       PPLICANT:
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COUNTRY: U.S.A.
ZIP: 20005-3934
                                                                                                                                                      STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
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                                                                                                                                                                                                             CITY: Washington
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APPLICATION NUMBER: US/C
FILING DATE: 14-NOV-1994
                                                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08340426D
                                                                                                                                                                                                                                 E: Sterne, Kessler, Goldstein & Fox P.L.L.C. 1100 New York Avenue, Suite 600
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1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                 de la Monte, s
Wands, Jack R.
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100.0%; Pred. No.
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                US/08/340,426D
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0.0018;
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                                                                                US-08-450-673C-57
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Best Local Similarity
Matches 37; Conserv
Query Match
Best Local Similarity
Matches 37; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21188 GCTAATTTTTGTATTTTTAGTAGAGACAGGGTTTCAC 21224
                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                              REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08
FILING DATE: 30-MAY-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                 LENGTH: 60 base pairs TYPE: nucleic acid STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C
STREET: 1100 New York Avenue, Suite 600
                                                                                                   TOPOLOGY: bo
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36,203
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                 0.1%; Score 37;
100.0%; Pred. No.
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   Mismatches
                 DB 4;
0.0018;
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0.0018;
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PCT-US95-17111A-57

Sequence 57, Application PC/TUS9517111A

GENERAL INFORMATION:
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Best Local Similarity
Matches 37; Conserv
                                                                                                                                                                       Sequence 69, Applicat Patent No. 5830670 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICATION NUMBER: 08/34
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                       TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: de la Monte, S
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neura
TITLE OF INVENTION: Detec
                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                 APPLICANT: de la Monte, S
APPLICANT: Wands, Jack R.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
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STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Ludwig, Steven R. REGISTRATION NUMBER: 36,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
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                                       ADDRESSEE:
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20005-3934
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Washington
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                                                                                                                                                                                                               Application US/08454557C
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               1100 New York Avenue, Suite 600
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                                     Sterne, Kessler, Goldstein & Fox P.L.L.C
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100.0%; Pred. No.
tive 0; Mismatci
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0.0018;
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RESULT 12
US-08-340-426D-69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 5948634
GENERAL INFORMATION:
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Best Local Similarity
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TELEFAX: (202) 371-25
INFORMATION FOR SEQ ID NO:
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                          APPLICATION NUMBER: US/08/340,426D FILING DATE: 14-NOV-1994 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Ludwig, Steven R. REGISTRATION NUMBER: 36,203
                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
COPPRANCE.
                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 371-2600
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APPLICANT: Wands, Jack R
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REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3840003
                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1100 New CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0 FILING DATE: 30-MAY-1995 CLASSIFICATION: 514
                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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                  371-2540
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100.0%; Pred. No.
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0.0017;
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SEQUENCE CHARACTERISTICS: LENGTH: 76 base pairs

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US-08-340-426D-69
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Sequence 69, App--
Sequence 69, App--
No. 5948888
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                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: (SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,673C
FILING DATE: 30-MAY-1995
CIASCIPTORITATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 530 ATTORNEY/AGENT INFORMATION:
              TITLE OF INVENTION:
                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washington STATE: D.C.
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                                                                                        Application PC/TUS9517111A
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                                         de la Monte, !
Wands, Jack R
                                                                                                                                                                                                                                                                                                                                                                        76 base pairs
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100.0%; Pr
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Detection of Alzheimer's Di
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0; Mismatches
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0.0017;
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0.0017;
                Disease
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Patent No. 5
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REGISTRATION NUMBER:
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US-08-454-557C-92
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Best Local Similarity
Matches 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: USEQUENCE CHARACTERISTICS:
LENGTH: 76 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21188 GCTAATTTTTGTATTTTTAGTAGAGACAGGGTTTCAC 21224
                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION: (202) 371-2600
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1 CURRENT APPLICATION DATA:
                                                                                                                                                                            ZIP: 20005-3934
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                       CITY: Washington STATE: D.C.
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STREET: 1
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FILING DATE: 14-NOV-199
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                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                     COUNTRY: U.S.A.
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20005-3934
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5830670
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                                          30-MAY-1995
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                                                          US/08/454,557C
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Pred. No.
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0.0017;
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36,203

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REFERENCE/DOCKET NUMBER: 0609.3840003

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2560

TELEPAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 92:
SEQUENCE CHARACTERISTICS:
LENGTH: 85 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
US-08-454-557C-92
                                                                                          Search completed: April 1, 2000, 04:07:52 Job time: 260334 sec
                                                                                                                                                                            Ouery Match 0.1%; Score 35; DB 3; Length 85; Best Local Similarity 100.0%; Pred. No. 0.0075; Matches 35; Conservative 0; Mismatches 0; Indels
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Minimum DB seq length: 8
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Perfect score:
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1 GTATATATCATGTGACTTG......AGGGGCAAAAGAAGAAGATCATG 30001
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13849.045 Million cell updates/sec
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em_est4: *
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em_est7: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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48	sult Query No. Score Match Length DB ID
8 0.2 1	% Query Match
102	Length
81	8
102 81 862983	ID
B62983 CIT-HSP-669	esult Query No. Score Match Length DB ID Description

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REFERENCE
AUTHORS
TITLE
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B62983/c
                                        COMMENT
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                                              JOURNAL
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Tel: 626 796 7066
Fax: 626 395 4901
                  Contact: Ung Jin Kim
CalTech Genome Research
California Institute of
Division of Biology, MS
                                                           Kim, U.-J., Adams, M.D. and Simon, M.I. Determination of clone end sequences
                                                                       Eukaryota; Metazoa; Chordata; Craniata;
Eutheria; Primates; Catarrhini; Hominida
1 (bases 1 to 102)
                                                                                                                        102 bp DNA GIT-HSP H GIT-HSP H GENOMIC SURVEY SEQUENCE. B62983
                                                                                                                                                                                                  Unpublished (1997)
                                                                                                                 B62983.1
                                                                                             Homo sapiens
ung@ash.tree.caltech.edu
                                                                                                                 GI:2636892
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N77004
AA873656
AI335049
HSMC09A06
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AA494273
AA228795
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                                                           end sequences
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147-75, Pasadena,
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                                                                                Hominidae;
                                                            of human
                                                                                                                                    GSS 21-JUN-1998 genomic clone 669F15,
                                                                                      Vertebrata;
                   CA 91125,
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AA457423 aa86b02.r
D25845 HUMGS04217
A1475290 t181c11
                                                            Bacterial Artificial
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AA129957 zn86h04.r
AA669571 ac18d10.s
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AQ276193 CITBI-E1-
R70733 Y146612.r1
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AA082835 zn21912.s
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AI088003 0024h05.x
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DEFINITION
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AUTHORS
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KEYWORDS
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JOURNAL
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Best Local (
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                                                                                                                                                                                                                          Eukaryota;
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                                                                                                                                                                                                                                                                  genomic
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48; Conservative
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                   /sex="Male"
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Venter, J.C.

Venter, J.C.

Use of BAC End Sequences for Sequen Unpublished (1997)

Contact: Mark Adams

Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0208

Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clones are available from Research Genetics (info@resgen.com). BA end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                              Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library PRCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
/note="Nector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
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/db_xref="GDB:5491647"
/db_xref="taxon:9606"
/clone="669F15"
                                                                                  /db_xref="taxon:9606"
/clone="RPCI-11-4A12"
/clone_1ib="RPCI-11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type="Sperm"
note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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                                                                                                                                                                     organism="Homo sapiens"
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                                                                                                                                               'db_xref="GDB:7501163"
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P RPCI-11 Homo
Y sequence.
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sapiens genomic
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2e-05;
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., Wible, C., de Jong, P.
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AA415364/c
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Best Local
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                                                                                                  24621 TCCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGCGCCCTGCCACC 24667
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                                                                              TCCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGCGCCTGCCACC
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                                                                                                                                                        . Similarity
47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lanfranchi,G., Muraro,T., Caldara,F., Pacchioni,B., Pallavic Pandolfo,D., Toppo,S., Trevisan,S., Scarso,S. and Valle,G. Identification of 4370 expressed sequence tags from a 3'-end-specific cDNA library of human skeletal muscle by DNA sequencing and filter hybridization genome Res. 6 (1), 35-42 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Via Trieste 75, 35121 Padua, Italy ABI Chromatograms and other information http://grup.bio.unipd.it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRIBI Biotechnology Centre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Apr 7, 1998 th Contact: Valle G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; M
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HSPD19063 HM3 Homo sapiens cDNA clone s4000074G04, mRNA sequence.
F29274
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                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                   ds cDNA was sonicated and size-selected in the range 350-550 bp. The 3' specific fragments were selected streptavidin coated magnetic beads, ligated to non-palindromic BstXI adapters, NotI digested and directionally cloned into BstXI-NotI cut pcDNAII vect a 19 c 38 g 16 t
                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="pectoral muscle (after mastectomy)", note="Vector: pcDNAII (Invitrogen); Site_1: BstXI; Site_2: Not1: The library was constructed by G. Lanfranchi. This library is not subtracted nor normalized. The first strand cDNA was primed with a biotinylated of the construction of the construction.
                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="s4000074G04"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="female
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="HM3"
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100.0%; Pred. No.
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Pred. No. 2e-05;
0; Mismatches (
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4.5e-05;
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AI305512/c
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JOURNAL
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                                                            ORGANISM
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                                                                                                                                                                                                                                                                                             74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The WashU-HHMI Mouse EST Project
Unpublished (1996)
On Jan 25, 1995 this sequence version replaced g1:637795.
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                        AI305512 82 bp n
qw72b02.x1 NCI_CGAP_Ov33
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1 (bases 1 to 74)

1 (bases 1 to 74)

Marra,M., Hillier,L., Allen,M., Bowles,M., Districh,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Lew,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 82)
                                                                                                                  AI305512
AI305512.1
                                                                                                                                                        mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
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                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: -40ml3 fwd.
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                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46
                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    were cloned into the MluI/SalI sites of a modified pBluescribe vector using commercial linkers (NEB). Average insert size: 1.2 kb."

5 c 17 g 6 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="Organ: embryo: Vector: pBluescribe (modified);
Site_1: MluI; Site_2: SalI; Cloned unidirectionally from
mRNA prepared from 13,500 2-cell stage embryos. Primer:
salI(dT): 5'.CGGTCGACCGTCGACCGTTTTTTTTTTTTTTT-3'. CDNAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Knowles Solter mouse
/tissue_type="embryo"
/dev_stage="2-cell"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="B6D2 F1/J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:790992"
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                                                                                                                    GI:3990403
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Pred. No.
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                                                                                                                                                                              Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: Robert_Strausberg@nih.gov

CDNA Library Preparation: David B. Krizman, Ph.D.

cDNA Library Arrayed by: I.M.A.G.E. Consortium, LLNL

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                  Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chiasoe,S., Dietrich,N., DuBugue,T., Favello,A., Gish,W., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Hawkins,M., Hultman,M., Kucaba,T., Lacy,J., Prange,C., Rifkin,L., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                     On May 18, 1995 this sequence version replaced Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                     Generation and analysis of 280,000 human expressed Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                    and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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www-bio.llnl.gov/bbrp/image/image.html
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National Cancer Institute, Cancer Genome Anat
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286 1800
286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1996587"
/clone="ib="NCI_CGAP_Ov33"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="adult"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="borderline ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="female"
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ocation/Qualifiers
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0.00045;
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Best Local Similarity
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ak64h01.s1 Barstead pa
IMAGE:1412689 3' simi
element;contains elem
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seg primer: -40M13 fwd, from Amersham.
                                                                                                                                                                                                                                                                                                              Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                 Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Josi Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. WashU-NCI human EST Project
Unpublished (1997)
                                                                                                                                                                                                                This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40ml3 fwd. Er from Amersham.

Location/Qualifiers
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism-"Homo sapiens"
/db_xref="taxon:9606"
/clone="MAGE:1412689"
/clone_1ib-"Barstead pancreas HPLRB1"
                                                         /sex="female"
/dev_stage="adult,
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
/clone="IMAGE:510094"
/note="Organ: pancreas; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Site_1: EcoRI; Site_2: Not
lst strand cDNA was primed with a Not I - oligo(dT) pr
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element KER repetitive element;, mRNA sequence
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Pred. No. 0.00043;
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                  24577 ATCTCGGCTCACTGCAAGCTCCGCCTCCCGGGTTCACGCCA 24617
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  50
  ATCTCGGCTCACTGCAAGCTCCGGCCTCCCGGGTTCACGCCA 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumor Gene Index
Unpublished (1997)
On May 18, 1998 this sequence version replaced gi:3137794.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
Life Technologies catalog #: 11547-015
DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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90 pp man...
wk06c11.x1 NCI_CGAP_Lym12 Homo sapiens cDNA clone image: 4%-
similar to contains Alu repetitive element;, mRNA sequence.
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National Cancer Institute, Cancer Genome Anat
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1 (bases 1 to 90)
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llarity 100.0%;
Conservative (
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                                                                                                                                                                                       /note="Organ: lymph node; Vector: pCMV-SPORT6; Site_1:
salr; Site_2: Not1; Cloned unidirectionally. Primer:
Oligo dT. Average insert size 1.25 kb. Life Technologies
catalog #: 11547-015"
a 29 c 27 g 21 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3']; double-stranded cDNA was ligated to Eco RI adaptors [AATTCGGATCCTTG], digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead. "
13 6 c 27 g 24 t
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/db_xref="taxon:9606"
/clone="IMAGE:2411540"
/clone_lib="NCI_CGAP_Lym12"
                                                                                                                                                                                                                                                                                                                             /tissue_type="lymphoma, follicular mixed small and large
                                                                                                                                                                                                                                                                                        /lab_host="DH10B"
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                                                                      Score 41; DB
;; Pred. No. 0.0
0; Mismatches
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Pred. No.
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0.0041;
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0.00085;
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HOmo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                AA129957 104 bp mRNA EST 27-NOV-1996 zn86h04.rl Stratagene lung carcinoma 937218 Homo sapiens cDNA clone IMAGE:565111 5' similar to contains Alu repetitive element;, mRNA
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Location/Qualiflers
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 97)
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ilarity 100.0%;
Conservative (
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//dev_stage="adult, 17 years"
//lab_host="DH10B"
//note="Organ: spleen; Vector: pT7T3D-Pac (Pharmacia) with
//note="organ: spleen; Vector: spleen; Site_2: not; lst
//note="organ: spleen; Vector: spleen; Site_2: not; lst
//note="organ: spleen; Vector: spleen; lst
//note="organ: spleen; ls
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/db_xref="taxon:9606"
/clone="IMAGE:1413466"
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Pred. No. 0.0039;
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 92.
Location/Qualifiers
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Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
Mardis,B., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J.,
Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41;
                                                             1 (bases 1 to 95).
Hiller,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                 ac18d10.s1 Stratagene ovary (#937217) Homo sapiens cDNA clone IMAGE:856819 3' similar to contains Alu repetitive element;, mRNA
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Fax: 314 286 1810
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         Unpublished
On Nov 6, 19
                                               WashU-NCI human EST Project
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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ilarity 100.0%;
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/db_xref="GDB:4594175"
/db_xref="taxon:9606"
/clone="IMAGE:565111"
ed (1997)
1997 this sequence version replaced g1:932677
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/tissue_type="lung carcinoma"
/cell_line="NCI-H69"
                                                                                                                                                                                                                                                              GI:2631070
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                       Email: est@watson.wustl.edu
Insert Size: 1093
High quality sequence stops: 65
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
INSERT Length: 1093
Sed priner: Promega -21m13
High quality sequence stop: 65.
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                                                                                                                                                                                                                                                                          Unpublished (1995)
On Apr 5, 1995 this sequence version replaced Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 96)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
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Fax: 314 286 1810
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         quality sequence stop: 65.
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/db_xref="taxon:9606"
/clone="IMAGE:856819"
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/sex="female"
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Mammalia;

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BASE COUNT
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AUTHORS
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AU072757
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Best Local S
Matches 39
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JOURNAL
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Best Local :
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                                                                                                                                                                                                                                                                                                                            University of Tsukuba
3-3-10 Ten-nodai, Tsukuba, Ibaraki 305, Japan
Email: d402hu@sakura.cc.tsukuba.ac.jp
PROJECT - Dictyostelium discoideum cDNA project
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AU072757 73 bp mRNA EST 24-JUN-1999
AU072757 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium
discoideum cDNA clone SSA765, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                     On Jun 5, 1998 this sequence version replaced g1:3188495.
Contact: Hideko Urushihara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Developmental cDNA in Dictyostelium discoideum (1999) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dictyostelium discoideum
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Similarity 100.0%;
40; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Urushihara,H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota;
                                                                                                     Similarity
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(bases 1 to 73)
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/clone_lib="Soares placenta Nb2HP"
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/dev_stage="slug"
0 c l g 26 t
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0.0083;
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AU038446
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AU038446.1
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                                                                                   AU038446 93 bp mRNA EST 29-MAR-1999
AU038446 Dictyostelium discoideum SS (H.Urushihara) Dictyostelium
discoideum cDNA clone SSH729, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1997)
on Jan 14, 1998 this sequence version replaced gi:1798653
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST
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Dictyostelium discoideum
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Location/Qualifiers
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Emmert-Buck, M.D., Ph.D.
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                  Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                      13
                                                                                                                                                                                                                                                                                                                                                                                                    /note-"Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 132376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                    Fatima Bonaldo. "
25 c 24 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
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Search completed: March 31, 2000, 22:13:51 Job time: 241085 sec
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2 (bases 1 to 93)

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length: 105
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-6790.570 Million cell updates/sec
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RESULT 1
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Sequence 57 from paten
AR051487
AR051487.1 GI:5974851
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HUMBRKFAB
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HUMALUANCB
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BTIGA45
HUMRSCB
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AR051521
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M36131 Human alpha
M36132 Human alpha
M36132 Human alpha
L39139 Human alpha
L36136 Homo sapien
L36843 Homo sapien
L36843 Homo sapien
A68621 Sequence 1
A807896 Human carci
A80781522 Sequence 17
L31159 Sequence 17
L310829 Human STS U
M15365 Human low d
X55240 M.musculus
L30244 Human STS U
M15365 Human low d
X55212 inter-Alu s
E09140 Squence 15
AF084962 Homo sapi
L31245 Sequence 15
AF084962 Homo sapi
L31364 Sequence 45
AF084114 Homo sapi
L31067 Human STS U
G37948 C4M78 Plasmo
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L31237 Sequence 14
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L31083 Human STS U
C37948 C4M78 Plasmo
M95703 Mouse micro
L31237 Sequence 14
M35654 D.melanogas
L31083 Human STS U
X85061 B.taurus co
K02284 Human Doly
G37817 SAH Plasmo
ARD SAH

K03556 Human low

29-SEP-1999

Minimum Maximum

Word size : Searched:

AR051487 Sequence AF087511 Homo sapi AR051499 Sequence

Description

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                                                 CTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGCTGGGATTACAGG 8783
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Homo sapiens clone ENaC+22 epithelial sodium channel alpha subunit
(SCNNIA) mRNA, alternatively spliced, partial sequence.
AF087511
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 66)
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                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 66)
Oh, Y. and Warnock, D.G.
Direct Submission
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                                                                                                                                                                           /gene="SCNN1A"
20 c
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/db_xref="taxon:9606"
/chromosome="12"
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14 c 15 g
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                                                                                                0.2%; Score 46; DB
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tive 0; Mismatches
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AR051499.1
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Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 80)
Kornreich,R., Bishop,D.F. and Desnick,R.J.
Alpha galactosidase A gene rearrangements
Identification of short direct repeats at
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de la Monte,S. and Wands,J
Neural thread protein gene
                                            Human alpha-galactosidase M36132
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J. Biol. Chem. 265, 9319-9326 (1990)
90264427
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         Fabry disease;
Human DNA.
                                  M36132.1 GI:179542
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                               Utah, Dept. of Human Genetics
2160 Eccles Institute of Human Genetics
Salt Lake City, UT 84112
e-mail: sts@corona.med.utah.edu
Primer A: AGTTCGAGACCAGCCTGGC
Primer B: AGGTGGCAGAAAATCGCATC
End to Label: Primer A
PCR Profile:
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L39139.1 GI:642101
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1 (Dases 1 to 69)

Gerken,S.C., Matsunami,N., Plaetke,R., Albertsen.H., Ballard,L., Melis,R., Lawrence,E., Moore,M., Holik,P.R., Carlson,M., Zhao,X., Robertson,M., Bradley,P., Elsner,T., Tingey,A., Lalouel,J.-M. and White,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alu-rich gene
J. Biol. Chem. 265, 9319-9326 (1990)
90264427
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                                                                                                                                                                                                                                                                                                                                                                                                   Submitted by: Utah Center for Human Genome Research University
                                                                                                                                                                                                                                                                                                                                                                                                                    Genetic and physical mapping of simple sequence repeat containing sequence tagged sites from the human genome Unpublished (1994)
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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10 sec. 62 C 10 sec. 72 C 20 sec.
58 C 10 sec. 72 C 20 sec. Mg++: 1.50 i
11 Acrylamide 7%, Formamide 32%, Urea 34%
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                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="19"
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/db_xref="taxon:9606"
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                               /evidence=experimental
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Homo sapiens 4000 year
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L36836.1 GI:556194
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43; Conserv
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Proc. Natl. Acad. Sci. U.S.A. 86 (6), 1939-1943 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (individual_isolate 4000 year Nekht-ankh) liver DNA.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                              Homo sapiens (individual_isolate 4000 year Nekht-ankh) liver DNA.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/isolate="4000 year old r.
/db_xref="taxon:9606"
/tissue_type="liver"
<1...>65
/tissue_type="liver
                  /organism="Homo sapiens"
/isolate="4000 year old
/db_xref="taxon:9606"
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17 c 21
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Nekht-ankh Alu repeat
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RESULCE, KALA, LATIONOV, V.L., KOUDTING, N.Y. and Perkins, TRANSFORMATION-ASSOCIATED RECOMBINATION CLONING PATENT: WO 9801573-A 15-JAN-1998;
US HEALTH (US)
                                                                                                                                  Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 103)

Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.

Alu RNA transcripts in human embryonal carcinoma cells. Model post-transcriptional selection of master sequences

J. Mol. Biol. (1992) In press

J. Mol. Biol. (1992) In press
                                                                                                                                                                                                                                                                                                                    HUMALCE221 103 bp ss-RNA
Human carcinoma cell-derived Alu RNA transcript,
M87896
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Sequence 1 from Patent WO9801573.
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/rpt_family="Alu"
a 18 c 23 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="unidentified"
/db_xref="taxon:32644"
12 c 13 g
                                                           /db_xref="taxon:9606"
/cell_line="NTera2D1"
/dev_stage="embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
               /tissue_type="carcinoma"
27 c 33 g 1
                                              /sex="male"
                                                                                                      organism="Homo sapiens"
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100.0%; Pred. No.
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GGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCAC 19054
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                             37; Conserv
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Kornrelch,R., Bishop,D.F. and Desnick,R.J.

Alpha-galactosidase A gene rearrangements causing Fabry disease:

Identification of short direct repeats at breakpoints in an
                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                Fabry disease; breakpoint junction; glycosphingolipid catabolism. Human DNA.
                                                                                                                                                                                                                                                                                                                                                                                                         HUMBRKFAC 80 bp DNA PRI Human alpha-galactosidase breakpoint region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent: US 5830670-A 92 03-NOV-1998;
Location/Qualifiers
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de la Monte,S. and Wands,J.R.
Neural thread protein gene expression and detection of Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unknown.
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Sequence 92 from patent
AR051522
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                               Conservative
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                                                                                                                                                                                                                            gene
                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
28 c 17 g 1
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27 c 25 g
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                            0.1%; Score 37; DB
100.0%; Pred. No. 3.4
tive 0; Mismatches
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GGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCAC

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 36
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 90)

Lehrman, M.A., Goldstein, J.L., Russell, D.W. and Brown, M.S.

Duplication of seven exons in LDL receptor gene caused by Alu-Alu recombination in a subject with familial hypercholesterolemia Cell 48 (5), 827-835 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="hgml; G00-119-362"
17 a 30 c 24 g 19 t
Chromosome 19p13.2-p13.1.
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Sequence 175 from patent
I31263
I31263.1 GI:1822054
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Alu repeat; low density lipoprotein receptor-1;
                                                                                                                                                                                Length polymorphisms in (dC-dA).sub.n.(dG-dT).sub.n sequences and method of using the same Patent: US 5582979-A 175 10-DEC-1996; Location/Qualifiers
                                                                                                                                                                                                                                           Weber, J.L
                                                                                                                                                                                                                                                                      Unclassified
                                                                                                                                                                                                                                                                                      Unknown
                                                                                                                                                                                                                                                                                                    Unknown.
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37; Conservative
                                                                                                                                                                                                                                                         (bases 1 to 40)
                                                   0.1%; Score 36; DB 5; I
llarity 100.0%; Pred. No. 1.1e-06;
Conservative 0; Mismatches 0;
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                                                                                                                                         /organism="unknown"
19 c 0 g
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/db_xref="taxon:9606"
/map="19p13.3"
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c US 5582979.
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REFERENCE
AUTHORS
TITLE
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ORIGIN
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ACCESSION
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KEYWORDS
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ORGANISM
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I31159/c
LOCUS
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Best Local Similarity
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            source
44 TGTATGTGTGTGTGTGTGTGTGTGTGTGTGTG
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Sequence
131159
131159.1
                                                                                                                                                     Length polymorphisms in (dC-dA).sub.nethod of using the same patent: US 5582979-A 71 10-DEC-1996; Location/Qualifiers
                                                                                                                                                                                                                            Unknown.
Unclassified
                                                                                                                                                                                                    Weber, J.L.
                                                                                                                                                                                                                                                     Unknown
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                                                                                                                    23
                                                                                                                                                                                                                                                                                                 46 bp DNA
71 from patent US 5582979.
                                                                                                                   /organism="unknown"
22 c 0 g
                                                                                                                                                                                                                                                                             GI:1821950
                                                        Score 36; DB 5; L
Pred. No. 1.1e-06;
                                                                                                                                                                                        in (dC-dA).sub.n.(dG-dT).sub.n sequences and
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Search completed: April 1, 2000, 10:12:16
Job time: 283685 sec

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Title:
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     GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Alu PCR primer 1. Repeat sequence fr Repeat sequence fr Sequence of a micr Microsatellite seq (dC-dA)n. (dG-dT)n Microsatellite seq (dC-dA)n. (dG-dT)n Microsatellite seq (dC-dA)n. (dG-dT)n Microsatellite seq Sequence of a micr Sequence of a micr Sequence of a micr Sequence of a microsatellite seq 
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RESULT T65743, ID T65743, ID T66 AC T

Homo sapiens. US5582979-A

10-DEC-1996. 21-APR-1989; 341562. 7765743; 197 (first entry)
17-JUN-1997 (first entry)
17-JUN-1997 (first entry)
Repeat sequence from polymorphic marker clone Mfd42.
Repeat sequence; genetic marker; primer; amplification; Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.

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1/c 165743 standard; DNA; 40

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	B 1; .33;	peat sequence; vector me; YAC; ss. VICES. VICES. EL, Resnick MA; ELL, Resnick MA; romosomes - by in viv ing yeast centromere, r recombination . The PCR primer used quence, which is used quence, which is used quence, which is used quence, which is not on in the invention. east artificial chron east artificial chron eic acids from a bac) the vector(s) into i e human DNA where on he methods large frag 13 G; 8 T;	
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Dr. Detection of polymorphic genetic markers of the form pr | Octobarre | Octo
DR WPI; 97-042299/04.

DR Dr betection of polymorphic genetic markers of the form protection of polymorphic genetic markers of the form produced form of polymorphic genetic acid mols. as primers produced form of polymorphic repeat sequences (dC-dA)n. (dG-dT)n which can be used as genetic contains the sequence (dC-dA)n. (dG-dT)n which can be used to detect these crown arkers. Primers based on these sequences can be used to detect these crown arkers. Primers based on these sequences can be used to detect these crown arkers. Primers based on these sequences can be used to detect these crown arkers. Primers based on these sequences can be used to detect these containing the repeat such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA). (dG-dT) crobe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers T65798-T66047. Those clones where the repeat sequence has been determined are shown in T65704-797. This repeat contains the repeat sequence is from the marker clone Mdf7 which contains the repeat contains the formula: (CA)20TA(CA)2.

Sequence 46 BP; 23 A; 22 C; 0 G; 1 T;
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Best Local S
Matches 36
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21-APR-1989; 341562.
21-APR-1989; US-341562.
05-SEP-1991; US-754551.
04-APR-1994; US-222177.
(MARS-) MARSHFIELD CLINIC.
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05-SEP-1991; US-754351.
04-APR-1994; US-222177.
(MARS-) MARSHFIELD CLINIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat sequence from polymorphic marker clone Mfd7. Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus;
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0; Mismatches
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RESULT
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        PPR PPR SWEET
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                                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                                             PT Polymorphic bowlne DNA markers - used in genetic identification,
PT gene mapping, and selective breeding
PS Table 7; Page 379; 517pp; English.

CC The sequence is that of a bowlne microsatellite sequence obtd.
CC 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.
CC One out of 50 clones cross-hybridised. Assuming independent
CC distribution of microsatellites and MboI sites, the frequency of
CC (T6)n >9 microsatellites in the bowlne genome is estimated at >100,
CC is summarised in the specification and indexed herein (see below).
CC The sequences upstream and downstream of the microsatellites sequence
CC were used to generate the required PCR primers for in vitro
CC amplification of the corresp. microsatellite (using the program
CC opTIPRIM). The microsatellites may be used to identify individuals,
CC for parentage testing, and in the genetic mapping of economic trait
CC loci, or genes involved the determinism of economic trait
CC see also Q33501-34437.
SQ Sequence 49 BP; 7 A; 0 C; 17 G; 25 T;
                                                                                                                                                                                                                                                                                                     Query Match
Best Local s
Matches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 36; Conser
(GENM-) GENMARK.
Georges M, Massey JM;
WPI; 92-284684/34.
Polymorphic bovine DNA
                                                     W09213102-A.
06-AUG-1992.
15-JAN-1992; U00340.
15-JAN-1991; US-642342.
                                                                                                                                                                                                                                                                28999 TGTATGTGTGTGTGTGTGTGTGTGTGTGTGTG 29034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UZ-FEB-1993 (first entry)
Microsatellite sequence from clone TGLA272.
PCR; selection; primers; OPTIPRIM; breeding;
genetic mapping; traits; amplification; ss.
Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENM-) GENMARK.
Georges M, Massey JM;
WPI; 92-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence of a microsatellite from clone TGLA68. PCR; selection; primers; OPTIPRIM; breeding; cattle; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-AUG-1992.
15-JAN-1992; U00340.
15-JAN-1991; US-642342.
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                                                                                                                                                                                     Q33870 standard; DNA;
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                                                                                                                                                                                                                                                                                                                    Similarity
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llarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                       Conservative
      bovine DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                 0.1%;
                                                                                                                                                                                        54 BP
      markers -
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                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                   Score :
                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
      used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36;
No.
                                                                                                                                                                                                                                                                                                                36;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
2.6;
                                                                                                                                                                                                                                                                                                                    2 DB
     genetic identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ٠
                                                                                                                                                                                                                                                     36
                                                                                                                                                                                                                                                                                                                    5
                                                                                                                                                                                                                                                                                                                               1:
                                                                                                                                     cattle;
                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 46;
                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           parentage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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T65737; T65737; Standard; DNA; 45 AC T65737;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PT gene mapping, and selective breeding
Table 7; Page 277; 517pp; English.

CC The sequence is that of a bovine microsatellite sequence obtd. by
CC Screening a library of bovine MboI DNA fragments of between
CC one out of 50 clones cross-hybridised. Assuming independent
CC distribution of microsatellites and MboI sites, the frequency of
CC (76)n >9 microsatellites in the bovine genome is estimated at >100,
CC (00. The sequence information for ca. 230 such bovine microsatellites
CC is summarised in the specification and indexed herein (see below).
CC The sequences upstream and downstream of the microsatellite sequence
CC amplification of the corresp. microsatellite (using the program
CC OFTIPRIM). The microsatellites may be used to identify individuals,
CC for parentage testing, and in the genetic mapping of economic trait
CC icol, or genes involved the determinism of economically important
CC can genes in cattle, to allow selective breeding.
Sequence 54 BP; 1 A; 0 C; 26 G; 27 T;
                                                                                                                                                                  Query Match
Best Local S
Matches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-AUG-1992.
24-JAN-1992; NL0018.
25-JAN-1991; NL-000132.
(INGE-) INCENY BV.
Uitterlinden AG, Vijg J;
WPI; 92-284683/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28999 TGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 29034
                                                                                                                                                                                                                                             Claim 6; Page 6; 31pp; English.

Primer PDJ33 is one of several primers which are preferred for use in amplifying inter-Alu regions of DNA. The amplified fragments are then subjected to 2-D electrophoresis on the basis of length and differences in base sequence. The resulting separation pattern is transferred to a filter for screening with a probe. The method can be used to detect genetic variation.

See Q27389-Q27404 and Q33141-Q33144.

Sequence 35 BP; 8 A; 10 C; 11 G; 6 T;
                                                                                                                                 8758 GCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCA 8792
                                                                                                                                                                                                                                                                                                                                                                                                                   Detection of genetic variation by 2-D electrophoresis of fragments - and hybridisation with labelled probes, carried on fragments consisting of inter-repeat sequences generated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inter-Alu specifi
Polymerase chain
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q27391 standard; DNA; 35 B
Q27391;
27-JAN-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11
                                                                                                   L
                                                                                                                                                                ch 0.1%; S
l Similarity 100.0%;
35; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 0.1%;
1 Similarity 100.0%;
36; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        lc primer PDJ33.
reaction; PCR; repetitive element;
                                                                                                                                                                  Score 35; DB; Pred. No. 4.9
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 36; ; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>.</u>
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                                                                                                                                                                                 DB 1
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2.5;
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                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 54;
                                                                                                                                                                                                 Length 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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RESULT
Q34053/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       per detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n - using novel nucleic acid mols as primers bisclosure; Column 9-10; 186pp; English.

CC The invention relates to the isolation of polymorphic repeat sequences to the isolation of polymorphic repeat sequences can having the sequence (dC-dA)n.(dG-dT)n which can be used as genetic markers. Primers based on these sequences can be used to detect these repeats, especially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease, commercial animal or plant breeding or pedigree analysis of containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA).(dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers T65798-T66047. Those clones where the repeat sequence has been determined are shown in T65704-797. This repeat sequence is from the marker clone Mdf36 which contains the repeat sequence analysing the formula: (AC)15AT(AC)6A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 35; Conserv
                                                                                                                                                                                                                                           06-AUG-1992.
15-JAN-1992; U00340.
15-JAN-1991; US-642342.
(GENM-) GENMARK.
GEOIGES M. MASSEY JM;
WPI; 92-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-DEC-1996.
21-APR-1989; 341562.
21-APR-1989; US-341562.
05-SEP-1991; US-754351.
04-APR-1994; US-222177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding gene mapping, and selective breeding Table 7; Page 352; 517pp; English.

The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 bp with an (AC)15 and a (T)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below).

The sequences upstream and downstream of the microsatellite sequence
                                                                                                                                                                                                                                                                                                                                                           Microsatellite sequence from clone TGLA438. FCR; selection; primers; OPTIPRIM; breeding; genetic mapping; traits; amplification; ss. Bos taurus.
WO9213102-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Repeat sequence from polymorphic marker clone Mfd36. Polymorphism; repeat sequence; genetic marker; primer; amplificati PCR; polymerase chain reaction; paternity; maternity; human; pedig linkage analysis; genetic disease; animal; plant; breeding; locus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q34053 standard; DNA; 62 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 97-042299/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US5582979-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hybridisation; chromosome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-JUN-1997 (first entry)
Repeat sequence from polym
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MARS-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.18;
required
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
PCR primers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
4.4;
                                                                                                                                                                                                                                                                                                                                                                                                                   cattle; parentage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amplification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pedigree;
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8888888
 RESULT
T66109,
ID T6
AC T6
DT 18
DE (0
KW P6
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                                                                                                                                                                    닭
                                                                                                                                                                                                                                                                                                                                                                                               gené mapping, and selective breeding

Pf gené mapping, and selective breeding

Ps Table 7; Page 225; 517pp; English.

The sequence is that of a bovine microsatellite sequence obtd. by

Cscreening a library of bovine MboI DNA fragments of between

Cone out of 50 clones cross-hybridised. Assuming independent

Cone out of 50 clones cross-hybridised. Assuming independent

Cdistribution of microsatellites and MboI sites, the frequency of

Cdistribution of microsatellites and MboI sites, the frequency of

Cdistribution of microsatellites and mboI sites, the frequency of

Cdistribution of microsatellites and mboI sites, the frequency of

Cdistribution of microsatellites and mboI sites, the frequency of

Cdistribution of microsatellites and bovine microsatellites

Si summarised in the specification and indexed herein (see below).

Che sequences upstream and downstream of the microsatellite sequence

Were used to generate the required PCR primers for in vitro

amplification of the corresp. microsatellite (using the program

Cdistribution of testing and in the seed to identify individuals,

Copribrily. The microsatellites may be used to identify individuals,
                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
T66109 standard; DNA; 47 BP.
T66109;
18-JUN-1997 (first entry)
(dC-dA)n.(dG-dT)n polymorphic d
Polymorphism; repeat sequence;
PCR; polymerase chain reaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           traits esp. in cattle, to allow selective breeding. See also Q33501-34437.
Sequence 62 BP; 21 A; 0 C; 10 G; 31 T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Georges M, Massey JM;
WPI; 92-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genetic mapping; traits; amplification; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amplification of the corresp. microsatellite (using the program OPTIFRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus
W09213102-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Microsatellite sequence f
PCR; selection; primers;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q33737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q33737 standard; DNA;
                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polymorphic bovine DNA markers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-AUG-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENM-) GENMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L5-JAN-1992;
L5-JAN-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                    10
                                                                                                                                                                      w
                                                                                                                                                                                                                                                                                                                                                  parentage testing, and in the genetic mapping of economic trait
i, or genes involved the determinism of economically important
its esp. in cattle, to allow selective breeding.
                                                                                                                                                                                                   TATGTGTGTGTGTGTGTGTGTGTGTGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATATATATATATATATATATATATATATACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35;
                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                      Q33501-34437.
39 BP; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U00340.
US-642342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                               0.1%; occ
100.0%; Pr
0;
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lymorphic double perfect repeat sequence.
sequence; genetic marker; primer; amplification;
reaction; paternity; maternity; human; pedigree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from clone TGLA153.
; OPTIPRIM; breeding; cattle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                    Score 34; DB Pred. No. 7.9 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                      0
C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            used in
                                                                                                                                                                                                                                                                                                                        17
                                                                                                                                                                                                                                                       7.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.;
                                                                                                                                                                                                                                                                                                                      G,
                                                                                                                                                                      36
                                                                                                                                                                                                   29034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genetic identification,
                                                                                                                                                                                                                                                      .
9;
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                                                                                                                                                                                                                                                                                                                      20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          parentage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                      0,
   pedigree;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                      0
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RESULT
Q34056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to the isolation of polymorphic repeat sequences containing the sequence (dc-dA)n. (dc-dT)n which can be used as genetic containing the sequence on these sequences can be used to detect these commercial sepecially for use in e.g paternity or maternity testing, commercial animal or plant breeding or pedigree analysis. Commercial animal or plant breeding or pedigree analysis.

CC onmercial animal or plant breeding or pedigree analysis.

CC interruptions and without adjacent repeats of another sequence; cc interruptions and without adjacent repeats of another sequence; cc interruptions and without adjacent repeats of another sequence; cc interruptions and without adjacent repeats of another sequence; cc interruptions and without adjacent repeats of another sequence; cc interruptions and without adjacent repeats of another sequence; cc interrupted by no more than 3 consecutive non-repeat bases; cc in ompore than 3 consecutive non-repeat bases from a run of at least compound perfect compound repeats which are defined as for the perfect compound repeats which are defined as for the perfect compound repeats which are defined as for the perfect compound repeats except that the runs of CA are interrupted.

CC This sequence with structure: A(A) 15TAGG(A)6, would be scored as 2 creates separate coeffect repeats seemences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-DEC-1996.
21-APR-1989; 341562.
21-APR-1989; US-341562.
05-SEP-1991; US-754351.
04-APR-1994; US-222177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29000 GTATGTGTGTGTGTGTGTGTGTGTGTGTGTGT
polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding Table 7; Page 353; 517pp; English.

The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MboI DNA fragments of between 250 and 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross hybridised. Assuming independent distribution of microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below).
                                                                                                                                                                                                                                                                                                                                                                                                                         Q34056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as Disclosure; Column 349-350; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hybridisation;
                                                                                                                                                                                                     Georges M, Massey JM;
WPI; 92-284684/34.
                                                                                                                                                                                                                                                                                                                                                genetic mapping;
                                                                                                                                                                                                                                                                                                                                                                 Microsatellite sequence from clone TGLA44.
PCR; selection; primers; OPTIPRIM; breeding;
                                                                                                                                                                                                                                                                                                                                                                                                      02-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 97-042299/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Weber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linkage analysis;
                                                                                                                                                                                                                                        (GENM-) GENMARK.
                                                                                                                                                                                                                                                           L5-JAN-1992;
L5-JAN-1991;
                                                                                                                                                                                                                                                                                               06-AUG-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MARSHFIELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                perfect repeat 47 BP; 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.1%;
nilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                       US-642342.
                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chromosome;
                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA;
                                                                                                                                                                                                                                                                                                                                                  traits; amplification;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLINIC
                                                                                                                                                                                                                                                                                                                                                                                                                                          56
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ВP
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Pred. No. 7.4
0; Mismatches
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7.4;
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                                                                                                                                                                                                                                                                                                                                                                   cattle; parentage
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                                                                                                                                                                                                                                                                                                     gene mapping, and selective breeding

Table 7; Page 304; 517pp; English.

The sequence is that of a bovine microsatellite sequence obtd. by

screening a library of bovine MboI DNA fragments of between

cone out of 50 clones cross-hybridised. Assuming independent

distribution of microsatellites and MboI sites, the frequency of

(T6)n >9 microsatellites in the bovine genome is estimated at >100,

000. The sequence information for ca. 230 such bovine microsatellites

is summarised in the specification and indexed herein (see below).

The sequences upstream and downstream of the microsatellite sequence

were used to generate the required PCR primers for in vitro

applification of the corresp. microsatellite (using the program

copyIPRIM). The microsatellites may be used to identify individuals,

for parentage testing, and in the genetic mapping of economic trait

loci, or genes involved the determinism of economically important

contraits each in cartile. To allow selective breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 34
                                                                                                                                                                                    Query Match
Best Local S
Matches 34
                                                                                                                                          29001 TATGTGTGTGTGTGTGTGTGTGTGTGTG 29034
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                              T26728 standard; cDNA to mRNA; T26728;
                                                                                                                                                                                                                                                                traits esp. in cattle, to allow selective breeding. See also Q33501-34437. Sequence 79 BP; 16 A; 0 C; 24 G; 39 T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Georges M, Massey JM;
WPI; 92-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genetic mapping; traits; amplification; ss
Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q33936 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polymorphic bovine DNA markers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-AUG-1992.
15-JAN-1992; U00340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Microsatellite sequence
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 Human
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                 22-OCT-1996 (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GENM-) GENMARK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             selection; primers;
                                                                                                                            TATGTGTGTGTGTGTGTGTGTGTGTGTGTG
 gene signature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34;
                                                                                                                                                                                    Similarity 100
34; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                0.1%; 5cc
100.0%; P7
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 HUMGS08978
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OPTIPRIM; breeding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                   Score 34;
Pred. No.
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Pred.
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No.
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6.2;
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7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genetic identification,
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Claim 2; Page 2158; 2245pp; Japanese.
Claim 2; Page 2158; 2245pp; Japanese.
Claim 3; Page 2158; 2245pp; Japanese.
Claim 4; Page 2158; Page 2
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Best Local S
Matches 34
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W09514772-A1.
01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19028 AGTGCTGGGATTACAGGCATGAGCCACTGCGCCC 19061
                       polymorphic bovine DNA markers - used in genetic identification, gene mapping, and selective breeding Table 7; Page 271; 517pp; English.

The sequence is that of a bovine microsatellite sequence obtd. by screening a library of bovine MDOI DNA fragments of between 250 and 500 bp with an (AC)15 and a C)15 oligonucleotide probe. One out of 50 clones cross-hybridised. Assuming independent distribution of microsatellites and MDOI sites, the frequency of (T6)n >9 microsatellites in the bovine genome is estimated at >100, 000. The sequence information for ca. 230 such bovine microsatellites is summarised in the specification and indexed herein (see below). The sequences upstream and downstream of the microsatellite sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genetic mapping;
Bos taurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-FEB-1993 (first entry)
Microsatellite sequence from clone TGLA261.
PCR; selection; primers; OPTIPRIM; breeding;
genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                            Georges M, Massey JM;
WPI; 92-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matsubara K, Oku
WPI; 95-206931/27
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human; cloning; mapping; non-biased library; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                               15-JAN-1992; U00340.
15-JAN-1991; US-642342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-AUG-1992.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (окив/) окиво к.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                             GENMARK.
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     generate
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       the
     required
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Pred. No.
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  PCR primers
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5.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cattle; parentage;
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      밁
                                                                                                                                                                                                                                                                                     PT gene mapping, and selective breeding
Fable 7; Page 271; 517pp; English.

CC The sequence is that of a bovine microsatellite sequence obtd. by
CC Screening a library of bovine MboI DNA fragments of between
CC Cone out of 500 bp with an (AC)15 and a (TC)15 oligonucleotide probe.
CC One out of 50 clones cross-hybridised. Assuming independent
CC Cone out of 50 clones cross-hybridised. Assuming independent
CC (T6)n >9 microsatellites and MboI sites, the frequency of
CC (T6)n >9 microsatellites in the bovine genome is estimated at >100,
CC out of the sequence information for ca. 230 such bovine microsatellites
CC is summarised in the specification and indexed herein (see below).
CC The sequences upstream and downstream of the microsatellite sequence
CC were used to generate the required PCR primers for in vitro
CC amplification of the corresp. microsatellite (using the program
CC opTIPRIM). The microsatellites may be used to identify individuals,
CC for parentage testing, and in the genetic mapping of economic trait
CC loci, or genes involved the determinism of economically important
CC see also Q33501-34437.
CC Sequence 44 BP; 22 A; 0 C; 0 G; 22 T;
                                                                                                                                     Query Match
Best Local Similarity
Matches 33; Conserv
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Best Local Similarity
Matches 33; Conserv
amplification of the corresp. microsatellite (using the program OPTIPRIM). The microsatellites may be used to identify individuals, for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding.

See also Q33501-34437.

Seguence 44 BP; 22 A; 0 C; 0 G; 22 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-FEB-1993 (first entry)
Microsatellite sequence from clone TGLA261.
PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
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WPI; 92-284684/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q33855 standard; DNA; 44 BP.
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15-JAN-1992; U00340
15-JAN-1991; US-642:
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ilarity 100.0%;
Conservative
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ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-642342.
                                                                                                                                  Score 33; DB; Pred. No. 13; 0; Mismatches
                                                                                                                                     0;
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Pred. No.
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Copyright (c) 1993 - 2000 Compugen Ltd
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/cgn2_6/ptodata/1/1na/6_COMB.seq:*
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US-08-454-577-71

US-08-222-177A-175

US-08-222-177A-157

US-08-222-177A-157

US-08-222-177A-157

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ALIGNMENTS

RESULT 1 US-08-454-557C-57 ; US-08-454-557C-57 STREET: 1100 New York Avenue, Suite 600 CITY: Washington STATE: D.C. COUNTRY: U.S.A. ZIP: 20005-3934 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1 CURRENT APPLICATION DATA: Sequence 57, Application US/08454557C Patent No. 5830670 Query Match Best Local : APPLICATION NUMBER: US/08/454,557C FILING DATE: 30-MAY-1995 CLASSIFICATION: 514 ATTORNEY/AGENT INFORMATION: NAME: Ludwig, Steven R. REGISTRATION NUMBER: 36,203 REFERENCE/DOCKET NUMBER: 0609.384000 TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 371-2500 GENERAL INFORMATION: APPLICANT: de la Monte, Suzanne APPLICANT: Wands, Jack R. TITLE OF INVENTION: heural Thread Protein Gene TITLE OF INVENTION: of Alzheimer's Disease NUMBER OF SEQUENCES: 121 TELEPHONE: (202) 371-2540 TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: 5 SEQUENCE CHARACTERISTICS: CORRESPONDENCE ADDRESS: LENGTH: 60 base pairs TYPE: nucleic acid STRANDEDNESS: both Local ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C. STREET: 1100 New York Avenue, Suite 600 ch 0.2%; 1 Similarity 100.0%; 46; Conservative both %; Score 46; DB %; Pred. No. 6.2 0; Mismatches 0609.3840003 . 6.2e-06; ches 0; DB 3; # Length 60; Expression and Detection

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Best Local Similarity
                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
NUMBER OF SEQUENCES: 121
CORRESPONDENCE ADDRESS:
COUNTRY: U.S.A.
ZIF: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
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                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                       TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection ITLE OF INVENTION: of Alzheimer's Disease
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20005-3934
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                                                                                                                                          E: Sterne, Kessler, Goldstein & Fox P.L.L.C 1100 New York Avenue, Suite 600
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                                                                                                                                                                                                                                                           Wands, Jack R
                                                                                                                                                                                                                                                                               de la Monte,
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14-NOV-1994
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Pred. No. 6.2e-06;
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Sequence 57, Application PC/TUS9517111A
GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/N
SOFTWARE: Patentin Release
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: 30-MAY-1995
CLASSIFICATION: 530
                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25363 GCTAATTTTTGTATTTTTAGTAGAGACAGGGTTTCACCGTGTTGGC 25408
                                                                                                             NAME: Ludwig, Steven R.
REGISTION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 066
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/3
FILING DATE: 14-NOV-1994
                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
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APPLICANT: Wands, Jack R
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                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS:
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                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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                                                                                               ELEPHONE:
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                : 60 base pairs
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1100 New York Avenue, Suite 600
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                                                                             (202) 371-2600
(202) 371-25
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Detection of Alzheimer's Disease
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n Release #1.0, Version #1.25
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US-08-454-557C-69; Sequence 69, App.; Patent No. 5830
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                                                                                                                                                                 RESULT
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                                                                                            Sequence 69, Application US/08340426D Patent No. 5948634 GENERAL INFORMATION:
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Best Local Similarity
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MEDIUM TYPE: Floppy disk
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REFERENCE/DOCKET NUMBER: 0609.3840003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
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                                                              APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
CORRESPONDENCE ADDRESS
                             TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease
            NUMBER OF SEQUENCES:
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ZIP: 20005-3934
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Wands, Jack R.
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Pred. No.
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US-08-450-673C-69
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                                                                                                                                           COUNTRY: U.S.A.

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/450,673C

FILING DATE: 30-MAX-1995
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
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ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                          CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease NUMBER OF SEQUENCES: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: de la Monte, S
APPLICANT: Wands, Jack R.
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STREET: 1100 New
CITY: Washington
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nes 46; Conservative (
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STREET: 1100 New York Avenue,
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Ludwig, Steven R.
Ludwig, Steven R.
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EDNESS: both
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1100 New York Avenue, Suite 600
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Pred. No.
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RESULT 9
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PCT-US95-17111A-69
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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
LENGTH: 76 base pairs
                                                                            25363 GCTAATTTTTGTATTTTTAGTAGAGACAGGGTTTCACCGTGTTGGC 25408
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                                                                                                                                                                                                                                                                                                                              NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 06:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340,426
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
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APPLICANT: Wands, Jack R.
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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20005-3934
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100.0%; Pred. No.
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Pred. No. 5.9e-06;
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RESULT 10
US-08-340-426D-92
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US-08-454-557C-92
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 92, Appl. Patent No. 594863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity Matches 39; Conserve
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                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (202) 371-25
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17462 GCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCC 17500
                               COMPUTER READABLE FORM:
MEDITM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
              CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
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LENGTH: 85 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection TITLE OF INVENTION: of Alzheimer's Disease NUMBER OF SEQUENCES: 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/0 FILING DATE: 30-MAY-1995 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Washington STATE: D.C.
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                                                                                                                                       COUNTRY: U.S.A. ZIP: 20005-3934
                                                                                                                                                                             CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08340426D
                                                                                                                                                                                                                       E: Sterne, Kessler, Goldstein & Fox P.L.L.C 1100 New York Avenue, Suite 600
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100.0%; Pred. No.
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US/08/340,426D
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Query Match
Best Local Similarity
Workshes 39; Conserve
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US-08-450-673C-92
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                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/450,673C
FILING DATE: 30-MAX-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                              TELEFAX: (202) 371-254
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 06
                                                                                                                                                                                                                              TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression and Detection
TITLE OF INVENTION: of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
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20005-3934
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                                                                                                                                                                                                               (202) 371-2600
(202) 371-2540
               0.1%; Score 39; DB llarity 100.0%; Pred. No. 0. Conservative 0; Mismatches
                                                                                                                 both
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Pred. No.
                                                                                                                                                                                                                                                                    0609.3840004
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        DB 4; Lc..
0.00086;
0;
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thes 0;
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                                              Length 85
               Indels
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             Gaps
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US-08-222-177A-175/c
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; Sequence 92, Application PC/TUS9517111A
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-US95-17111A-92
                                                                                                                                                                                                      Sequence 175, Application US/08222177A Patent No. 5582979
                         GENERAL INFORMATION: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUEN
NUMBER OF SEQUENCES: 460
CORRESPONDENCE ADDRESS:
ADDRESSEE: DeWitt Ross & Stevens, S.C.
STREET: 8000 Excelsior Drive, Suite 401
                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340
FILING DATE: 14-NOV-1994
ATTORNEY_AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,20
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 85 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: de la Monte, Suzanne
APPLICANT: Wands, Jack R.
TITLE OF INVENTION: Neural Thread Protein Gene Expression
TITLE OF INVENTION: Detection of Alzheimer's Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1100 New CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 36,203 REFERENCE/DOCKET NUMBER: 06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
ZIP: 20005-3934
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Wisconsin
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                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                       AND METHODS OF USING SAME
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

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US-08-222-177A-71/c
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Best Local Similarity
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Patent No. 558297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2106
TELEFAX: (608) 831-2106
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28999 TGTATGTGTGTGTGTGTGTGTGTGTGTGTGTG 29034
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                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
FILING DATE: 21-APR-1989
                                                                                                                                                                                                                                                                                                                     APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 460
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dewitt Ross & Stevens, S.C.
STREET: 8000 Excelsior Drive, Suite 401
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36 TGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
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CLASSIFICATION: 435
                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 53717-1914
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                                                                                                                                                                                                                                                                                    STATE: Wisconsin
                                                                                                                                                                                                                                                                                                         CITY: Madison
                                                                                                                   APPLICATION NUMBER:
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0.0086;
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mueting, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 110.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOR COMPATION OF THE FORM O
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CORRESPONDENCE ADDRESS:
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LENGTH: 46 base pairs
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
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APPLICANT: Chung, Ming-yi
APPLICANT: Zoghbi, Huda Y.
TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 54 base pairs
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119 No. 5741645th Fourth Street, Suite 203
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0.1%; Score 36; DB 2;
ilarity 100.0%; Pred. No. 0.0081;
Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                             AA082835 59 bp mRNA
zn21g12.s1 Stratagene neuroepithelium
cDNA clone IMAGE:548134 3' similar to
element; mRNA sequence.
AA082835 GI:1624910
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, 1
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
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Fax: 314 286 1810
Email: est@watson.v
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Washington University School of Medici 4444 Forest Park Parkway, Box 8501, St Tel: 314 286 1800
              Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or f Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.} Seg primer: T7
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Zhao,S., Adams,M.D., Nier
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Use of BAC End Sequences
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40M13 fwd. from Amersham.
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Inpublished (1997)
On May 1, 1997 this sequence version replaced
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Ph.D.

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GCAP clone distribution information can be
found through the I.M.A.G.E. Conscrtium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                          Seq primer: -40UP from Gibco.
Location/Qualifiers
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  Score 52;
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CIT-HSP-669F15.TP CIT-HSP Homo sapiens genomic clone 669F15,
                                                                         genomic survey sequence.
B48914
B48914.1 GI:2601151
                                                                                                                       B48914 103 bp DNA RPCI11-4A12.TP RPCI-11 Homo sapiens
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                                                                                                                                        B48914
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Class: BAC ends.
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Fax: 626 395 4901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Calfech Genome Research Lab
California Institute of Technology
Division of Biology, MS 147-75, Pasadena, CA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                             Homo sapiens
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/clone="669F15"
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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/db_xref="GDB:5491647"
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Adams,M.D., Rounsley,S.D., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P.
                                                                                                                                                                                                            Lanfranchi,G., Muraro,T., Caldara,F., Pacchioni,B., Pallavic: Pandolfo,D., Toppo,S., Trevisan,S., Scarso,S. and Valle,G. Identification of 4370 expressed sequence tags from a 3'-end-specific cDNA library of human skeletal muscle by DNA sequencing and filter hybridization sequences. 6 (1), 35-42 (1996)
                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 91)
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Seq primer: SP6
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Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or fi
Research Genetics (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The Institute for Genomic Research 9712 Medical Center Dr., Rockville, Tel: 301 838 0200
Fax: 301 838 0208
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Contact: Mark Adams
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Use of BAC End Sequences for Sequence-Ready Map Building
                                   Via Trieste 75, 35121 Padua, Italy ABI Chromatograms and other information http://grup.bio.unipd.it.
                                                                                                      Oniversity of Padua
                                                                                                                                                On Apr 7, 1998 this sequence Contact: Valle G.
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/db_xref="GDB:7501163"
/db_xref="taxon:9666"
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/clone=lib="RPCI-11"
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RPCII1 Human Male BAC Library"
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                                                                                                                                              Email: est@watson.wustl.edu
Insert Size: 614
High quality sequence stops: 70 Source: IMAGE Consortium, clone is available royalty-free through LLNL; contact the Consortium (info@image.llnl.gov) for further information.
Insert Length: 614 Std Error: 0.00
Seq primer: M13RP1
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                                                                                                                                                                                                                                                                                                       Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                           Contact: Wilson RK
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                                                                                                        quality sequence stop: 70.
Location/Qualifiers
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llarity 100.0%; F
Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="pectoral muscle (after mastectomy)"
/note="Vector: pcDNAII (Invitrogen); Site_1: BstXI;
Site_2: NotI; The library was constructed by G.
Lanfranchi. This library is not subtracted nor normalized.
The first strand cDNA was primed with a biotinylated oligo-dT-NotI primer
(5'-biotin-AACCCGGCTGGAGCGGCCGCTTTTTTTTTTTTTTTTT-3'). The ds cDNA was sonicated and size-selected in the range 350-550 bp. The 3' specific fragments were selected by streptavidin coated magnetic beads, ligated to non-palindromic BstXI adapters, NotI digested and directionally cloned into BstXI-NotI cut pcDNAII vector."

18 a 19 c 38 g 16 t
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/db_xref="taxon:9606"
/clone="s4000074G04"
/clone_lib="HM3"
/organism="Homo sapiens"
/db_xref="GDB:487980"
/db_xref="taxon:9606"
/clone="IMAGE:119691"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="female"
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Pred. No.
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24-MAR-1995

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              17445 GGGGTTTCACCATGTTAGCCAGGATGGTCTCGATCTCCTGACCT 17488
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GGGGTTTCACCATGTTAGCCAGGATGGTCTCGATCTCCTGACCT
                                                        44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N84707 70 bp mRNA
J0579F Human fetal heart, Lambda ZAP Express
clone J0579 5' similar to REPETITIVE ELEMENT
                                                                                                                                                                                                                                                                                                                                                         Fax: 4169785650
Email: liewcc@utcc.utoronto.ca
Seg primer: GAAATTAACCCTCACTAAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                          Banting Institute, 100 College St., Tel: 4169788758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Eutheria; Primates;
1 (bases 1 to 70)
                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Laboratory Medicine and Pathobiology University of Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Liew CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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47; Conservative
                                                                      Similarity
                                                        Conservative
                                                                                                                                                24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from fetal heart
                                                                                                                                          /lab_host="E. coli XL1-Blue"
/note="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2:
/note="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2:
XhoI: mRNA was purified from human fetal hearts (8-10
weeks). cDNA was synthesized using a XhoI-Oligo dT
adaptor-primer. EcoRI adaptors were ligated, followed by
digestion with XhoI, for directional cloning into
predigested lambda ZAP Express."

a 18 c 15 g 13 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="J0579"
                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Stratagene lung (#937210)"
/sex="male"
                                                                                                                                                                                                                                                                 /clone_lib="Human fetal heart, Lambda ZAP Express"
                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
                                                                     0.2%;
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Pred. No.
                                                                     Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (1996)
                                                        Mismatches
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                                                                   DB 25;
0.0011;
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                                                                                   Length ?0;
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S Homo sapiens cDNA
T ALU, mRNA
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                                                                                                                                                                                                                                                                                                                             19018 GGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCGCCC 19061
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                                                                                                                                                                                                                                                                                                              80
                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                              GGCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACTGCGCCC
                                                                                                                                                                                                                                                                                                                                                                                44;
Okubo,K., Fukushima,A., Yoshii,J., Niiyama,T., Kojima,Y., Yoshinari,H., Arimoto,J. and Matsubara,K.
Gene expression of human promyelocytic cell line HL60 before and
                                                                   Eukaryota; Metazoa;
Eutheria; Primates;
                                                                                                     Homo sapiens
                                                                                                                                         EST
                                                                                                                                                                                                       HUMGS01971 Human promyelocyte Homo sapiens cDNA clone mp0383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Via Trieste 75, 35121 Padua, Italy ABI Chromatograms and other information http://grup.bio.unipd.it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRIBI Biotechnology Centre University of Padua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Jun 5, 1998 this sequence version replaced gi:3188834 Contact: Valle G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lanfranchi,G., Muraro,T., Caldara,F., Pacchloni,B., Pallavicini,A., Pandolfo,D., Toppo,S., Trevisan,S., Scarso,S. and Valle,G. Identification of 4370 expressed sequence tags from a 3'-end-specific cDNA library of human skeletal muscle by DNA sequencing and filter hybridization genome Res. 6 (1), 35-42 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HSPD10834 HM3 Homo sapiens
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                                                                                                                                                       D20989.1
                                                   (bases 1 to 87)
                                                                                                                                                                                         sequence.
                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    streptavidin coated magnetic beads, ligated to non-palindromic BstXI adapters, NotI digested and directionally cloned into BstXI-NotI cut pcDNAII vector."

1 21 c 19 g 22 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="s4000013A06"
/clone_lib="HM3"
                                                                                                                                                         GI:504809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'sex="female"
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                                                                                                                                                                                                                           87 bp
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                                                                                                                                                                                                                                                                                                                                                                                              Score 44;
Pred. No.
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nes 43; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Hiller, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptce, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. WashU-NCI human EST Project
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA835205 101 bp mRNA EST 23-FEB-1998 ak64h01.sl Barstead pancreas HPLRB1 Homo sapiens cDNA clone IMAGE:1412689 3' similar to contains Alu repetitive element; contains element KER repetitive element; mRNA sequence.
                                                                                                                                                                                                                                                    Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Seq primer: -40ml3 fwd.ET from Amersham.
                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1997)
On Nov 29, 1993 this sequence version replaced g1:636226
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 101)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     after induction of differentiation. A new application of CDNA sequencing Unpublished (1993) Contact: Okubo,K., Fukushima,A., Yoshii,J., Niiyama,T., Yoshinari,H., Arimoto,J. and Matsubara,K. Institute for Molecular and Cellular Biology
                                                                                                                                                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
               /note="Organ: pancreas; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRI; Site_2: NotI; lst strand cDNA was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    promyelocyte.
                                                                                                                        /sex=":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="mp0383"
                                                                                    /dev_stage="adult, 34 years"
/lab_host="DH10B"
                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1412689"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Human promyelocyte"
/note="Female, adult, cell_line = HL60, cell_type
promyelocyte. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
/clone_lib="Barstead pancreas HPLRB1"
                                                                                                                                                                                                                                     Location/Qualifiers
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Matches 41
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 90)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Tumor Gene Index
Tumor Gene Index
Tumor Gene Index
Topublished (1997)
On May 18, 1998 this sequence version replaced g1:3137794.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: Robert_Strausberg@nih.gov
Life Technologies catalog #: 11547-015
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: -40UP from Gibco.
Location/Qualifiers
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llarity 100.0%;
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1 36 c 27 g 24 t
                                                                                                                                                                                                 /clone="IMAGE:2411540"
/clone_lib="NCI_CGAP_Lym12"
/tissue_type="lymphoma, folicell"
                                                                                                                                                                                                                                                                                                                                                                                                             /organism-"Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                          /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90 bp mRNA EST 30-AUG-1999 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2411540 3' contains Alu repetitive element;, mRNA sequence.
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Pred. No.
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Best Local S
Matches 41
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                                                                                                         AUTHORS
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Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1407381.
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA780764 91 bp mRNA EST 05-FEB-1998 ac68f12.sl Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:867791 3' similar to contains Alu repetitive element;, mRNA
                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 102)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Tumor Gene Index
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1309483.
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40ml3 fwd. ET from Amersham.
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/db_xref="taxon:9606"
/clone="IMAGE:867791"
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RESULT 15
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cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
cDNA Sequencing by: Washington University Genome Sequencing Cencent Clone distribution: NCI-CGAP clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 103)

Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linh; Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H. Gilden, M. and Venter, J.C.
Use of a random BAC End Sequence Database for Sequence-Ready | Building (1998)
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                                                                                                                                                                                                                   Unpublished (1998)
Other_GSSs: CIT-HSP-2163G1.TF
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Location/Qualifiers
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-41m13 fwd. ET from Amersham
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. 0.0076;
ches 0;
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                                                                             20850,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bass, S., Linher, K.,
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BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13 Reverse
Class: BAC ends.
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